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(54) Title: P_{2X} RECEPTORS (PURINOCEPTOR FAMILY)			
(57) Abstract <p>The P_{2X} receptor of ATP has been cloned and expressed by recombinant DNA technology, so the receptor can be prepared free from other ATP receptors. The P_{2X} receptor enables antibodies to be prepared and is useful in screening compounds for use in a variety of diseases and conditions, including epilepsy, cognition, emesis, pain (especially migraine), asthma, peripheral vascular disease, hypertension, diseases of the immune system, irritable bowel syndrome and premature ejaculation.</p>			

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P2X RECEPTORS (PURINOCEPTOR FAMILY)

This invention relates to the P_{2X}-purinoceptor, its preparation and uses.

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The P_{2X}-purinoceptor is a ligand-gated ion channel; that is, the receptor itself forms an ion channel which opens when extracellular adenosine 5'-triphosphate (ATP) binds to the receptor. There are five other classes of neurotransmitter receptors (nicotinic acetylcholine, glutamate, glycine, GABA_A and 5-HT₃); these form a structurally related superfamily of ligand-gated ion channels (Barnard, *Trends Biochem. Sci.* 17, 368-374, (1992)). The P_{2X}-receptor now identifies a new family of this type of receptor. The unique structure of this receptor, the widespread distribution of this receptor throughout the body, and the numerous physiological roles this receptor may play, make it an important protein that can be used to identify new, therapeutically effective, compounds for the treatment of a number of pathological states.

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In 1929 the eminent physiologist Szent-Gyorgyi described powerful cardiovascular actions of extracellular purine nucleosides (e.g. adenosine) and nucleotides (e.g. ATP) (Drury & Szent-Gyorgyi, *J. Physiol.* 68 213-237 (1929)), but it was not until 1972 that pharmacological evidence was provided to suggest the existence of distinct receptors for extracellular ATP (ie. that recognise ATP but not adenosine) (Burnstock, *Pharmacological Reviews* 21 509-581 (1972)). The seminal and subsequent work on this area by Burnstock and colleagues was largely unaccepted throughout the 1970s and early 1980s until the development of a range of relatively selective ligands

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and techniques for directly measuring ATP release overwhelmingly substantiated Burnstock's hypothesis (Barnard et al., *Trends Pharmacol. Sci.* 15 67-70 (1994)). In the past four or five years, unequivocal evidence for the role of ATP as a neurotransmitter has been provided for sympathetic control of blood flow to the intestine and smooth muscle tone (contractility) in genitourinary tissue such as vas deferens, bladder and ureter (Barnard et al. (*loc. cit.*) and Evans & Surprenant, *Brit. J. Pharmacol.* 106 242-249 (1992)). Substantial indirect evidence also exists for the role of ATP as a neurotransmitter in a number of distinct neurones in the spinal cord, autonomic ganglia and certain nuclei in the central nervous system (Bean, *Trends Pharmacol. Sci.* 15 67-70 (1992), Evans et al., *Nature* 357, 503-505 (1992) and Edwards et al., *Nature* 359 144-147 (1992)).

Purinoceptors are classified as P_1 (adenosine as ligand) and P_2 (ATP as ligand). The P_2 receptors are subclassified into two broad types - those that are 7-transmembrane receptors that couple to G-proteins (P_{2Y} , P_{2U} , P_{2T} , and perhaps P_{2Z}) and those that form a directly gated ion channel (P_{2X}). Pharmacological and/or physiological evidence for subtypes of each of these types of receptors exists. The most recent nomenclature for these receptors is shown below.

	P_{2X}	P_{2Y}	P_{2Z}
Type	Ligand-gated channel	G-protein coupled	Non-selective pore
Subtype	P_{2X1} , P_{2X2} , P_{2X3}	P_{2Y1} , P_{2Y2} , P_{2Y3}	

Various P_2 receptors have previously been cloned. P_{2Y1} was cloned by the Barnard/Burnstock group (Webb et al., *FEBS Lett.* 324 219-225 (1993)) based on homology with

other 7-TM G-protein coupled receptors. This group used PCR technology and primers based on conserved domains of the second and sixth transmembrane regions to screen a mammalian brain cDNA library and, with final success, an embryonic chick whole-brain cDNA library.

P_{2Y2}/P_{2U} was cloned by the Julius laboratory (Lustig et al., *Proc. Nat'l. Acad. Sci. USA* 90 5113-5117 (1993)) by expression cloning in the oocyte from cDNA obtained from a NG108-15 neuroblastoma cell line.

P_{2Y3}/P_{2T} was also obtained by the Barnard/Burnstock group using the same probes and embryonic brain cDNA library used to obtain the P_{2Y1} receptor (Barnard et al., *Trends Pharmacol. Sci.* 15 67-70 (1994)).

However, as yet, cloning of the P_{2X} receptor has remained an elusive goal. The prior cloning exercises undertaken for the other P_2 receptors do not provide an adequate lead to enable the P_{2X} receptor to be cloned. First, all the above purinoceptors are G-protein coupled 7-TM proteins. Their myriad functions (like those of all 7-TM receptors) occur through G-protein activation of one or more second messenger systems. There are over 200 currently identified proteins which belong to this 7-TM/G-protein coupled family. Agonists at these receptors activate cascades of intracellular transduction pathways, often involving several enzymes; the response of the cell is inherently slow (several seconds to minutes) and changes in excitability are subtle if they occur. In contrast, the P_{2X} receptor is a fundamentally different type of purinoceptor that incorporates an ion channel. Activation of P_{2X} receptors is rapid (milliseconds), has predominately local effects, and brings about immediate

depolarisation and excitation.

Secondly, the tissue distribution of the P_{2X} receptor is distinctly different from other purinoceptors, and the physiological roles differ from other purinoceptors.

One of the principal established ways to clone a receptor is based on sequence relatedness of the nucleotides that encode the amino acids of the receptor protein; it depends on there being a fairly high level of homology between a known sequence and that of the unknown receptor. This method was used to clone the P_{2Y1} form (above). Several laboratories, including that of the applicants, invested significant effort in obtaining the P_{2X} receptor using PCR techniques and primers based on conserved regions of various ligand-gated ion channels (ie. nicotinic ACh, GABA, glutamate, 5-HT₃). This approach failed. With hindsight, this failure can be rationalised, as it can now, but only now, be seen that the structure of the P_{2X} receptor bears no homology with any of these ligand-gated ion channels. For the same reason, approaches based on fragment hybridisation would not succeed.

However, by adopting a different approach, it has now been found possible to clone the P_{2X} receptor, and it is on this achievement that the present invention is in part based.

According to a principal aspect of the present invention, there is provided a recombinant or isolated DNA molecule encoding a P_{2X} receptor, wherein the receptor:

- (a) has the amino sequence shown in Figure 1, Figure 2, Figure 3 or Figure 4; or

(b) is substantially homologous to the sequence shown in Figure 1, Figure 2, Figure 3 or Figure 4;

or a fragment of such a DNA molecule, which fragment includes at least 15 nucleotides taken from nucleotides 1 to 813 shown in Figure 1, the full nucleotide sequences shown in Figures 2 and 3, or from nucleotides 1 to 1744 shown in Figure 4.

The sequence shown in Figure 1 is a cDNA sequence that encodes a rat vas deferens P_{2X} receptor. This sequence is 1837 bases in length and encodes a protein of 399 amino acids. As was determined after the receptor was cloned, approximately one half of the protein-encoding sequence, from nucleotides 814 onwards, had been discovered previously but the function of the previously cloned sequence was not known except that it appeared to be implicated in apoptotic cell death (Owens *et al.*, *Mol. Cell. Biol.* 11 4177-4188 (1991)); the Owens *et al.* sequence lacks a translation initiation site and could not be made into protein. (In Figure 1, the upstream portion of the reported sequence of Owens *et al.*, namely PQLAHGCYPCPPHR, which is not shared with the P_{2X} receptor, is shown for comparative purposes and does not form part of the invention.)

Preferably the Figure 1 sequence fragments are taken from nucleotides 1-810. Often the Figure 4 sequence fragments are taken from nucleotides 1-777.

The sequence shown in Figure 2 is a cDNA sequence that encodes a rat superior cervical ganglion P_{2X} receptor.

The sequence shown in Figure 3 is a cDNA sequence that encodes a rat dorsal root ganglion P_{2X} receptor.

5 The sequence shown in Figure 4 is the cDNA sequence that encodes a human P_{2x} receptor. The cDNA was isolated from the human urinary bladder using a rat P_{2x} probe. It is 2643 bases long and encodes a 399 amino acid protein having an amino acid sequence which is highly homologous with the amino acid sequence of the rat P_{2x} receptor isolated from rat vas deferens and with the rat P_{2x} receptors isolated from a rat superior cervical ganglion and from a rat dorsal root ganglion. Recently we have become aware of an expressed sequence tag corresponding to residues 1745-1933 (Proc. Natl. Acad.Sci. USA 91,10645-10649 (Oct. 1994).

10 Sequences which are substantially homologous to the Figure 1, Figure 2, Figure 3 or Figure 4 amino acid sequence include those which encode proteins having at least 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% homology in increasing order of preference. A protein having at least 99% homology with the amino acid sequence of Figure 1, Figure 2, Figure 3 or Figure 4 will have no more than four
15 amino acid variations from such a sequence. Preferred substantially homologous sequences include P_{2x} sequences from other species. Thus for the rat P_{2x} receptor sequences a preferred substantially homologous sequence is a human P_{2x} sequence. One method of determining sequence homology is disclosed in WR Pearson and DJ Lipman, *Proc Natl Acad Sci USA* 85:2444-2448 (1988).

20 Fragments may of course be larger than 15 nucleotides. Fragments encoding substantially the whole of the P_{2x} rat receptors or human receptor may be expected to share the biological activity of the receptor, or at least some of its biological activities. Shorter fragments may be useful for encoding one or more
25 selected domains of the receptor, or simply as probes for detecting or identifying other useful DNA sequences, including those encoding substantially homologous proteins. Fragments of

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at least 20, 30 or 50 nucleotides may be more frequently of use than shorter ones.

5 DNA molecules of the invention are useful for a number of purposes. First, and not least, the P_{2X} cDNA shown in Figure 1, in Figure 2, in Figure 3 and in Figure 4 enables the relevant proteins to be expressed in living cells. This would not be possible with fragments of the cDNA. However not only are fragments of DNA within the
10 scope of the invention, for the various purposes mentioned above, but also genomic and other sequences of DNA (including synthetic DNA and "minigenes", which include at least one, but not all, of the introns naturally present in the gene) are included within its
15 scope. cDNA sequences encoding the rat receptor proteins or human P_{2X} receptor protein may be preferred in some circumstances because such sequences are smaller than either genomic or minigene DNA and therefore more amenable to cloning manipulations. The P_{2X} receptor
20 protein can be stably expressible in chinese hamster ovary (CHO) cells, as will be described below.

Still on the subject of expression, while it would be possible to express genomic DNA in eukaryotic cells, it
25 is much more difficult to manipulate the DNA for insertion into host cells due to the larger size that commonly results from introns. The size is particularly important for the expression of RNA; very long cRNAs -- the size of whole genes -- are difficult to make in
30 sufficient quantity. On the other hand, expression from RNA is much preferred at least for the investigation of ion channel proteins, because the *Xenopus* oocyte is sufficiently large to be studied easily by electrophysiological methods.

Secondly, the cDNA sequences encode proteins that, in their predicted folding within the membrane, differ from other known proteins. This is advantageous because, based on historical precedent, this will lead to the
5 discovery of a large family of related proteins and these may have functional roles unrelated to signalling mediated by ATP.

Thirdly, knowledge of the protein sequences encoded by
10 rat and human P_{2X} cDNA allows the development of molecular models that predict the detailed disposition within the membrane. It further allows the correctness of such models to be determined by expression of mutagenised proteins. These two approaches are advantageous because
15 they may permit the molecular design of complementary therapeutic agents that activate or block the receptor.

Fourthly, the P_{2X} cDNA sequences allow the distribution of the RNA that encodes this receptor, as well as the
20 receptor protein itself, to be mapped in human tissues. RNA distribution can be determined by *in situ* hybridisation. Such hybridisation studies are disclosed in the present examples. Knowledge of a deduced amino acid sequence from cDNA allows synthetic peptides to be
25 made that can be used to generate antibodies that selectively recognise a P_{2X} receptor. Thus a P_{2X} protein can be mapped by immunohistochemistry. This may suggest novel therapeutic applications for drugs that activate or block the P_{2X} receptor, that can not be predicted on the
30 basis of less sensitive current methods for localising the receptor (radioactive ligand binding).

Fifthly, rat P_{2X} cDNA is advantageous because it can allow
35 the isolation of a closely related cDNA from human tissue.

Sixthly, the isolation of the human P_{2X} cDNA clone will enable a human genomic clone to be obtained. It is probable that mutations of this gene will be discovered that lead to human genetic disease. The analysis of such mutations may lead to appropriate treatments of diseases or disorders caused by such mutations.

In one aspect of the present invention rat vas deferens P_{2X} receptor was cloned by a method which does not require prior inference about structure. Tissues were chosen that were believed to be rich in the RNA for the receptor of interest. A number of tissue sources were tried but they did not provide RNA that led to ATP responses in oocytes. Eventually, vas deferens was chosen. From extracted polyadenylated RNA, a cDNA library or bank that corresponds as far as possible to the DNAs in the tissue was constructed. It was not assured, either before work began or until it was satisfactorily completed, that a satisfactory cDNA library in which the rat P_{2X} gene was represented could be constructed; nevertheless, this was achieved in plasmid pBKCMV.

An individual clone within the library that contains the rat vas deferens P_{2X} cDNA of interest was detected by progressive fractionation of the library; at each step the fraction was tested to determine whether RNA made from it can direct the formation of the protein of interest. More specifically, RNA was transcribed in vitro from the cDNAs in the library (approximately 2 million) and the RNA ("cRNA") mixture was injected into immature *Xenopus* oocytes. cRNA is very susceptible to inadvertent enzymatic degradation, so all procedures were carried out under sterile conditions. The cDNA pools were made by the miniprep procedure and therefore

contained large amounts of *E. coli* RNA; this difficulty was overcome by precipitating any RNA before the cRNA was transcribed.

5 Detection of the protein can in principle be done by radioactive ligand binding or by a functional response. The activation of G proteins in the *Xenopus* oocyte and the subsequent cellular response was used to obtain the P_{2Y2}/P_{2U} receptor. In the present work, a decision was
10 made to use the opening of the integral ion channel of the P_{2X} as the response. Individual oocytes were screened two days after injection to determine whether they had made P_{2X} receptor protein in their membrane. This was done by recording the current flowing across the oocyte
15 membrane when ATP (30 μ M) was applied to the outside of the oocyte; if the P_{2X} receptor has been produced, a small transient current would be expected. However, testing for expression of the receptor was not straightforward, as some batches of oocytes exhibit
20 responses to ATP because they naturally express other kinds of ATP receptor. This difficulty was overcome as follows: when an oocyte responded to ATP with the expected current this was further tested by blockade with a P_{2X} receptor antagonist (suramin). The cDNA fraction
25 that gave led to the positive response in such an oocyte was further divided, and each fraction was again tested. Such progressive fractionation led to isolation of a single clone. The insert in the plasmid was sequenced; the sequence is shown in Figure 1. This sequence was
30 used to design PCR primers which were used in the cloning of cDNA encoding a P_{2X} receptor from a rat superior cervical ganglion (see Figure 2). A similar procedure was then used in the cloning of cDNA encoding a P_{2X} receptor from a rat dorsal root ganglion (see Figure 3).

DNA in accordance with the invention will usually be in recombinant or isolated form and may be in the form of a vector, such as a plasmid, phagemid, cosmid or virus, and in some embodiments contains elements to direct
5 expression of the protein, for example in a heterologous host. Non-expressible vectors are useful as cloning vectors.

Although DNA in accordance with the invention may be
10 prepared synthetically, it is preferred that it be prepared by recombinant DNA technology. Ultimately, both techniques depend on the linkage of successive nucleotides and/or the ligation of oligo- and/or poly-nucleotides.

15 The invention enables, for the first time, P_{2X} receptor to be prepared by recombinant DNA technology and hence free from protein with which it is naturally associated or contaminated (such as the P_{2U} or, particularly, P_{2Y}
20 receptor, or other ATP receptors or binding proteins), and this in itself forms another aspect of the invention. The protein will generally be associated with a lipid bilayer, such as a cell, organelle or artificial membrane. P_{2X} receptor prepared by expression of DNA in
25 accordance with the first aspect may be glycosylated, but does not have to be. Generally speaking, receptor proteins and ion channels that are glycosylated will also function after carbohydrate removal or when expressed in cells that do not glycosylate the protein. However,
30 there are often important quantitative differences in the function between the glycosylated and non-glycosylated protein. In the case of the rat vas deferens P_{2X} receptor, we believe that the native protein is glycosylated because it has a molecular weight of 62 kd

when purified from the rat vas deferens, as compared to the molecular weight of 45 kd for the cloned protein. Similar results were obtained for the human P_{2X} receptor (see later).

5

There are also several asparagine residues in the extracellular domain that are likely sites of sugar attachment.

10

Knowledge of the amino acid sequence of a P_{2X} receptor enables the protein or peptide fragments of it to be prepared by chemical synthesis, if required. However, preparation by expression from DNA, or at least translation from RNA, will usually be preferred.

15

Particularly useful peptide fragments within the scope of the invention include epitopes (which may contain at least 5, 6, 7, 10, 15 or 20 amino acid residues) of the P_{2X} receptor which are immunologically non-cross reactive with the RP-2 polypeptide disclosed in Owens et al., loc. cit.

20

A P_{2X} receptor, and fragments of it, can be used to prepare specific polyclonal and monoclonal antibodies, which themselves form part of the invention. Polyclonal and monoclonal antibodies may be prepared by methods well established in the art. Hybridoma and other cells expressing monoclonal antibodies are also within the invention.

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RNA encoding a P_{2X} receptor, transcribable from DNA in accordance with the invention and substantially free from other RNAs, also forms part of the invention, and may be useful for a number of purposes including hybridisation

studies, *in vitro* translation and translation in appropriate *in vivo* systems such as *Xenopus* oocytes.

5 The invention also relates to host cells transformed or transfected with a vector as described above. Host cells may be prokaryotic or eukaryotic and include mammalian cells (such as COS, CHO cells and human embryonic kidney cells (HEK 293 cells)), insect cells, yeasts (such as *Saccharomyces cerevisiae*) and bacteria (such as *Escherichia coli*).
10 Host cells may only give transient expression of the receptor, as in the case of COS cells, but for preference the host cells are stably transfected with the vector. Host cells which appropriately glycosylate the receptor are preferred. A CHO cell line
15 or any other cell line that stably expresses a P_{2X} receptor can be used for electrophysiological, calcium-influx, calcium-imaging and ligand-binding studies. Host cells which do not express the receptor may still be useful as cloning hosts.

20 A P_{2X} receptor prepared by recombinant DNA technology in accordance with the invention has a number of uses, either *in situ* in a membrane of the expression host or in *in vitro* systems. In particular, the receptor can be
25 used as a screen for compounds useful in a variety of human (or other animal) diseases and conditions, as will now be briefly described. Such compounds include those present in combinatorial libraries, and extracts containing unknown compounds (e.g. plant extracts).

30 **Epilepsy** Epilepsy results from overexcitation of distinct neurones in specific regions of the brain, in particular in the hippocampus. Functional ATP P_{2X} receptors are known to be present in some hippocampal

neurones. If the P_{2X} receptors are expressed on inhibitory interneurons, then receptor agonists would be therapeutically useful. If the receptor is expressed on principal (pyramidal or granule) cells, then receptor antagonists will be useful. If will now be possible to determine which classes of neuron express the receptor.

Cognition Hippocampal neurones respond to ATP by activation of a P_{2X} receptor; these areas are of primary importance to cognition. It is now possible to determine the cellular localisation of the P_{2X} receptor with in the hippocampus; depending on this localisation, either agonists or antagonists might be effective to enhance memory.

Emesis The acute trigger for emesis is rapid contraction of smooth muscle of the upper gastrointestinal tract. Activation of ATP P_{2X} receptors present on smooth muscle of the GI tract, in particular the stomach and trachea, results in strong, rapid muscle contractions. P_{2X} -antagonists selective for visceral smooth muscle could be useful for emesis. Furthermore, P_{2X} receptors are known to be expressed in the nucleus of the tractus solitarius (Ueno et al., *J. Neurophysiol.* 68 778-785 (1992)) and may be involved in transmission from primary visceral afferents; this could be blocked by selective P_{2X} antagonists.

Pain First, P_{2X} receptors are expressed in dorsal horn neurones of the spinal cord. Activation of these neurones by ATP causes fast depolarizing, excitatory responses (Jahr & Jessell, *Nature* 304 730-733 (1983)); if a component of the transmission from nociceptive fibres is mediated by ATP then this could be blocked by

a P_{2X} antagonist. Secondly, ATP is one of the most noxious substance known when applied intradermally. This is because it activates directly the peripheral terminals of small diameter nociceptive fibres; it is known that the cell bodies in the dorsal root ganglion express P_{2X} receptors. A P_{2X} antagonist would be a peripherally active analgesic, and is likely to be effective in migraine.

Asthma Bronchial smooth muscles contract in response to activation of P_{2X} receptors. This may occur in response to ATP released from sympathetic nerves, or from local immune cells. P_{2X} antagonists may help to prevent stimulus-evoked spasms of bronchial smooth muscle and thereby reduce the frequency and/or severity of asthmatic attacks.

Peripheral vascular disease It is becoming clear that ATP and not noradrenaline is the primary vasoconstrictor neurotransmitter in small resistance arteries - those that comprise over 70% of total peripheral resistance. This has been shown for many vessels (Westfall et al., *Ann. N.Y. Acad. Sci.* 603 300-310 (1991)). A selective antagonist could be used for local collateral vasodilation.

Hypertension Hypertension that is associated with increased sympathetic tone could be treated with P_{2X} receptor antagonists, because ATP is a major excitatory transmitter to many resistance vessels in several species including man (Westfall et al., *loc. cit.* and Martin et al., *Br. J. Pharmacol.* 102 645-650 (1991)).

Diseases of the immune system A molecule identical to part of the P_{2X} receptor has been cloned from thymocytes that have been induced to die (Owens et al., *loc. cit.*).

The selective expression in these conditions implies that a molecule closely related to the P_{2X} receptor plays a role in the apoptosis that is an integral part of the selection of immunocompetent cells. The molecule described by Owens et al. (RP-2) was incomplete and could not have been translated into protein. The cloning of the P_{2X} receptor will now allow the isolation of full length RP-2 clones, their heterologous expression and the determination of their functional roles.

Irritable bowel syndrome ATP is an important transmitter to the smooth muscles of the intestinal tract, particularly in the colon. It is also a transmitter between neurons in the enteric nervous system, by activating P_{2X} receptors (Galligan, *Gastroenterology*, in press). Antagonists at P_{2X} receptors may therefore have utility in the management of this condition.

Premature ejaculation This could be prevented by preventing stimulus-evoked contraction of vas deferens smooth muscle. P_{2X} receptors are highly expressed in this tissue; antagonists at this site would prevent vas deferens contractility during sympathetic excitation.

Cystitis P_{2X} receptors may be implicated in increased bladder sensitivity in patients with cystitis. Thus antagonists of such P_{2X} receptors may be useful in treating cystitis.

Useful agonists and antagonists identified as described above also form an aspect of the invention.

The cloning of the hP_{2X} receptor is an important aspect of the present invention. hP_{2X} is the first human member of

a multigene family of ionotropic purinoceptors. Its strong similarity with P_{2X} , isolated from rat vas deferens and with P_{2X} isolated from rat superior cervical ganglion or from rat dorsal root ganglion, suggests that it is a human homolog of the rat proteins. The present inventors have found that differences between these two sequences are nearly all conservative substitutions of hydrophilic residues. Surprisingly, hP_{2X} has only 41% identity with the other reported P_{2X} receptor, that from rat PC12 cells (Brake et al, New structural motif for ligand-gated ion channels defined by an ionotropic ATP receptor Nature 371: 519-523 (1994)). The PC12 derived receptor was proposed to have a similar membrane topography and shares the conserved spacing of cysteine residues, indicated for the two smooth muscle sequences in Figure 5.

The computed molecular weight of the hP_{2X} polypeptide (45 kd) agrees with that of the *in vitro* translation product when made in absence of pancreatic microsomal membranes. A larger product, 60 kd, produced in presence of microsomes suggests glycosylation and supports the idea of a central extracellular domain. The predicted hP_{2X} protein thus has the general features of other cloned members of this family (Valera et al, A new class of ligand-gated ion channel defined by P_{2X} receptor for extracellular ATP Nature 371: 516-519 (1994); Brake - *supra*): a large, cysteine-rich extracellular central domain flanked by two transmembrane spans and short internal N- and C-termini.

The distribution of the hP_{2X} mRNA was examined by northern blot analysis. Hybridisation of a principal 2.6 kb species was seen in all RNA samples tested, with the exception of brain. A smaller, 1.8 kb band, observed in

spleen, and lung mRNAs could be due to a shorter 3' untranslated portion of the mRNA, as occurs for P_{2X} mRNA from the rat vas deferens. The hybridisation observed in thymus, lung, spleen and liver RNA may reflect the content of smooth muscle in those organs. However, hP_{2X} is likely to have roles in other cell types, as demonstrated by its presence in adrenal gland, and the hemopoietic cell line HL60. The strong induction of hP_{2X} mRNA by HL60 differentiation may reflect a parallel observation in rat in which the smooth muscle form of P_{2X} mRNA can be induced in immature thymocytes by dexamethasone (RP2 mRNA; Owens et al, Identification of mRNAs associated with programmed cell death in immature thymocytes *J J Molec Cell Biol* 11: 4177-4188 (1991)).

The present invention has enabled the first comprehensive pharmacological characterization of a cloned P_{2X}-purinoceptor to be made. The time course of the responses to ATP and the sensitivity to α,β , γ -methylene ATP are similar to those reported for the native hP_{2X} in urinary bladder (Inoue & Brading, Human, pig and guinea-pig bladder smooth muscle cells generate similar inward currents in response to purinoceptor activation *Br J Pharmacol* 103: 1840-1841 (1991)). Thus the functional properties of some native P_{2X} purinoceptors can be obtained by the expression of a single molecular species. The agonist induced current recorded from oocytes expressing the hP_{2X} clone gives a direct measure of the activation of P_{2X}-purinoceptors in a system with low levels of endogenous ectonucleotidase activity. The agonist profile 2MeSATP \geq ATP $>$ α,β , γ -meATP for hP_{2X} is similar to that of the cloned rat vas deferens P_{2X}-purinoceptor. The high potency of α,β , γ -meATP in whole tissue studies (α,β , γ -meATP \gg 2MeSATP \geq ATP) probably reflects, its

resistance to ectonucleotidases.

5 The concentration-effect curves for ATP, 2MeSATP and 2-chloro-ATP were superimposable, indicating that these particular substitutions at the 2' position on the adenine ring do not affect agonist binding to the P_{2X} -purinoceptor. The agonist activity of AP_5A is likely to be because diadenosine phosphates (AP_5A , and AP_6A) released from the platelets can act as vasoactive agents through activation of P_{2X} -purinoceptors.

Preferred features of each aspect of the invention are as for each other aspect, *mutatis mutandis*.

15 The invention will now be illustrated by the following examples. The examples refer to the accompanying drawings, in which:

20 FIGURE 1 shows DNA and amino acid sequences of the rat vas deferens P_{2X} receptor as determined in Example 2. (SEQ ID NO 4).

25 FIGURE 2 shows DNA and amino acid sequences of a rat superior cervical ganglion P_{2X} receptor, as determined in Example 11. (SEQ ID NO 5).

30 FIGURE 3 shows DNA and amino acid sequences of a rat dorsal root ganglion P_{2X} receptor, as determined in Example 12. (SEQ ID NO 6).

FIGURE 4 shows DNA and amino acid sequences of a

human P_{2X} receptor as determined in Example 6. (SEQ ID NO 7)

5 FIGURE 5 shows the alignment of the predicted amino acid sequence of hP_{2X} with the rat vas deferens P_{2X} , and *in vitro* translation of hP_{2X} protein.

10 TM1 and TM2 filled boxes indicate the hydrophobic regions and boxed amino acids indicate the differences between the two sequences,

o indicates conserved cysteine residues.

15 * Indicates potential sites of N-glycosylation.

20 FIGURE 6 shows an SDS-PAGE analysis of ^{35}S -methionine labelled hP_{2X} protein. Lanes 1 and 2 show *in vitro* coupled transcription/translation of pBKCMV- hP_{2X} cDNA in the absence and presence of microsomal membranes, respectively.

25 FIGURES 7 AND 8 show Northern analyses of the hP_{2X} cDNA, wherein:

A) FIGURE 7 shows Northern blot with 8 μg of total RNA from differentiated HL60 cells.

30 0 indicates HL60 cells without treatment;
PMA2 and PMA3 indicate respectively cells treated 2 days, and 3 days with PMA;
DMSO indicates cells treated 6 days with DMSO;
dcAMP indicates cells treated 5 days with dibutryl

cAMP;

UB indicates 100 ng of polyA⁺ RNA from human urinary bladder; and

5 B) FIGURE 8 shows distribution of hP_{2X} in human tissues. Lanes contained 1 µg polyA⁺ RNA except for the urinary bladder which contained 0.2 µg of polyA⁺ RNA.

10 FIGURES 9, 10 and 11 show the response of oocytes expressing hP_{2X} to purinoceptor agonists, wherein:

15 A) FIGURE 9 shows traces which show inward currents evoked by ATP, 2 me SATP and α,β, me ATP (0.1, 1, and 100 µM). Records for each agonist are from separate oocytes;

20 B) FIGURE 10 shows concentration response relationships of full P_{2X}-purinoceptor agonists. Data are expressed relative to the peak response to 100 µM ATP; and

25 C) FIGURE 11 shows concentration response of partial P_{2X}-purinoceptor agonists. Data are fitted with a Hill slope of 1 (n = 4-8).

30 FIGURES 12 and 13 show the effects of P2-purinoceptor antagonists of hP_{2X} mediated responses, wherein;

A) FIGURE 12 shows concentration response curves for ATP in the presence of the P2-purinoceptor

agonist suramin (1, 10 and 100 μ M) (n = 4 for each point); and

5 B) FIGURE 13 shows concentration dependence of suramin, DIDS, PPADS and P5P in inhibiting the response to 10 μ M ATP (n = 4 for each point).

10 FIGURE 14 shows the results of the functional characterisation of rat superior ganglion P_{2X} receptors (as encoded by clone 3, described in Example 10). These experiments provided electrical recordings from transfected HEK293 cells.

15 Top left: Superimposed currents evoked by ATP (30 μ M) during the time are indicated by the bar. Holding potential was changed from -70 to 20 mV.

Top right: Peak current as a function of membrane potential.

20 Bottom left: Superimposed currents evoked by ATP, from 1 to 300 μ M.

Bottom right: Concentration-response curves for ATP and $\alpha\beta$ methylene-ATP (points are mean \pm s.e. mean for 5 - 8 experiments).

25 FIGURE 15 shows the inhibition of currents caused by various substances acting on the clone 3 form of the P_{2X} receptor (as described in Example 11), compared with PC12 and human bladder forms in HEK293 cells.

30 Top: inhibition by suramin.

Middle: inhibition by PPADS.

Bottom: inhibition by pyridoxal 5-phosphate.

EXAMPLES(i) RAT VAS DEFERENS P_{2X} RECEPTOR

5

EXAMPLE 1 Cloning of the Rat vas deferens P_{2X} Receptor

Total RNA was isolated by the guanidinium isothiocyanate method (Sambrook et al., "Molecular Cloning: A Laboratory Manual" Cold Spring Harbor Laboratory Press, 10 second edition (1989)) from vas deferens of 4 weeks old Sprague-Dawley male rats, and the poly A+ RNA was subsequently purified by oligo(dT)-cellulose. First strand cDNA primed with the sequence 5'-
15 GAGAGAGAGAGCGGCCGCTTTTTTTTTTTTTTTT-3' (SEQ ID NO 1) was synthesised with SUPERScript™ (BRL, Gaithersburg, MD, USA). After conversion of the cDNA to double stranded (Gubler & Hoffman, Gene 25 263-269 (1983)) EcoRI linkers were ligated to the cDNA, and the product was digested with NotI. The EcoRI-NotI cDNA of 1.3 to 9 kb was isolated by
20 gel electrophoresis, and a unidirectional library was constructed by ligation of the cDNA to pBKCMV (Stratagene, San Diego, CA, USA) digested with the same enzymes. The library was electroporated into E. coli DH10B cells and divided in 24 pools of 8×10^4 clones.
25 The plasmid DNA from the pools was prepared by minialkaline lysis followed by LiCl precipitation (Sambrook et al., loc. cit). NotI-linearised cDNA was transcribed in vitro with T3 RNA polymerase in the presence of the cap analogue m7GpppG (Sambrook et al.,
30 loc. cit). The in vitro transcribed RNA (cRNA) was concentrated to 4 mg/ml.

EXAMPLE 2 Sequencing of the Rat vas deferens P_{2X} Receptor cDNA

The cDNA insert was sequenced the exonuclease method (Henikoff Meth. Enzymol. 155 156-164 (1987)). The sequence is shown in Figure 1.

EXAMPLE 3 Functional characterisation of the Rat vas deferens P_{2X} Receptor cDNA in Oocytes

50 nl (200 ng) of RNA was injected into defolliculated *Xenopus* oocytes. After incubation for 2-6 days at 18°C, the oocytes were assayed for ATP-evoked currents by a two-electrode voltage clamp (GENECLAMP™); one electrode is to hold the voltage constant (at -100 mV), and the other is to measure the currents. A cDNA pool which showed ATP induced currents was subdivided to obtain a single clone (P_{2X}). Electrophysiological measurements were done at -100 mV, in a perfusion medium containing 96 mM NaCl, 2 mM KCl, 1.8 mM CaCl₂, 1 mM MgCl₂, 5 mM Hepes pH 7.6, and 5 mM sodium pyruvate. For dose-response curves and suramin inhibition, oocytes were injected with 100 ng P_{2X} cRNA, and all recordings were performed at -60 mV, with Ba²⁺ substituted for external Ca²⁺ to prevent activation of endogenous Ca²⁺-activated Cl⁻ currents. Microelectrodes (0.5-2 MΩ) were filled with 3M KCl.

EXAMPLE 4 Functional characterisation of the Rat vas deferens P_{2X} Receptor cDNA in HEK 293 Cells

HEK 293 cells were transfected by the lipofectin method (Felgner et al., Proc. Nat'l. Acad. Sci. USA 84 7413-7417 (1987)) with P_{2X}-plasmid. DNA concentration used was 1 mg/2 ml medium placed into a 35 mm petri dish containing four 11 mm diameter coverslips on which HEK cells were placed at 10,000 cells per coverslip. Cells were exposed to lipofectin/DNA for 6 h and recordings made 16 - 36 h

later; 40 - 60% of cells from which recordings were made exhibited P_{2X} responses. Currents were recorded from HEK 293 cells using whole-cell recording methods and the Axopatch[™] 200 amplifier (Axon Instruments); patch pipettes (5 M Ω) contained (mM) Cs or K aspartate 140, NaCl 5, EGTA 11, HEPES 5. The external solution was (mM) NaCl 150, KCl 2, CaCl₂ 2, MgCl₂ 1, HEPES 5 and glucose 11; the pH and osmolarity of both solutions were maintained at 7.3 and 305 mosmol/l respectively. All recordings performed at room temperature. Data acquisition and analysis were performed using pCLAMP[™] and Axograph[™] software (Axon Instruments). Solutions for experiments examining calcium permeability of ATP currents in HEK cells contained (mM): internal solution NaCl 150, HEPES 5, CaCl₂ 0.5 and EGTA 5 (free calcium concentration about 5 nM); external sodium solution NaCl 150, glucose 11, histidine 5, CaCl₂ 2; external calcium solution CaCl₂ 115, glucose 11 and histidine 5. The pH and osmolarity of the solutions were 7.4 and 295 mosmol/l respectively. For single channel measurements, a GENECLAMP[™] 500 amplifier and outside-out recording methods were used (Adelman et al., Neuron 9 209-216 (1992)). Wax-coated patch pipettes (5 - 10 M Ω) contained (mM) K-gluconate 115, HEPES 5, BAPTA 5 and MgCl₂ 0.5, external solution was 96 mM NaCl, 2 mM KCl, 1.8 mM CaCl₂, 1 mM MgCl₂, 5 mM Hepes pH 7.6, and 5 mM sodium pyruvate. ATP was applied by U-tube typically for 1 s; data was sampled at 5 kHz in 2 s segments beginning 300 ms prior to onset of agonist (ATP) application and filtered at 1 kHz.

30

EXAMPLE 5 Transfection of the Rat vas deferens P_{2X} Receptor cDNA into CHO and HEK293 Cells

CHO cells were stably transfected by a method used for other ion channels (Claudio, Meth. Enzymol. 207 391-408

- (1992)). Transfection was confirmed by a) electrophysiological recording and b) radioligand binding. ATP and other agonists (up to 30 μ M) caused rapidly desensitising inward currents in 14 of 14 CHO cells stably transfected, and had no effect in 45 of 45 non-transfected cells. [3 H] α β methyleneATP binding was more than 600 cpm per million transfected cells with less than 80 cpm nonspecific binding.
- 5
- 10 Stable transfection of HEK293 cells was also achieved. This was confirmed by electrophysiological recording.

(ii) HUMAN P_{2X} RECEPTOR

The materials and methods used in the human P_{2X} receptor examples are set out below:

5

In Vitro translation *In vitro* coupled transcription/translation were performed using Promega's TNT Coupled reticulocyte lysate Systems with or without 2 μ l of canine pancreatic microsomal membranes (Promega). μ g
10 Circular pBKCMV-hP_{2X} (0.5 ug) was transcribed with the T3 RNA polymerase as described in the system manual in a 25 μ l reaction for 2 h at 30°C. Synthesized proteins (5 μ l) were analysed by SDS-PAGE and autoradiography.

15

Differentiation of HL60 cells HL60 cells (human promyelocytes ATCC CCL240) were passaged twice weekly in RPMI-1640 supplemented with 25 mM HEPES, 2 mM Glutamax II, and 10% heat-inactivated fetal calf serum (GIBCO BRL). For each experiment 33×10^6 cells were resuspended
20 at 2.5×10^5 cells/ml in medium containing either phorbol myristate acetate (100 nM), 1.1% DMSO, or dibutyryl cAMP (200 μ M) (SIGMA) for the indicated times.

25

Northern blot analysis PolyA⁺ RNAs were obtained from Clontech Laboratories Inc. (Palo Alto) except for the urinary bladder and HL60 mRNA which were prepared as described (Valera et al (1994) - *supra*). Samples were quantified by measuring the O.D. at 260 nm, and by staining the membrane with methylene blue. The RNA were
30 fractionated on a 1% agarose - 6% formaldehyde gel and electroblotted to a non-charged nylon membrane (BDH). Prehybridisation at 68°C was performed for 6 hours in hybridisation buffer (50% formamide, 5X SSC, 2% blocking buffer (Boehringer Mannheim), 0.1% lauroylsarcosine,

- 0.02% SDS). Hybridisation was overnight at 68°C in fresh hybridisation buffer with a digoxigenin-UTP labelled riboprobe (100 ng/ml) corresponding to the entire hP_{2x} sequence. The membrane was washed at 68°C; twice in 2X SSC + 0.1% SDS, and twice in 0.1X SSC + 0.1% SDS. Chemiluminescent detection of hybridisation was carried at room temperature as follows: the membrane was rinsed 5 min in buffer B1 (0.1 M maleic acid, 0.15 M NaCl, pH 7.5), saturated for 1 hour in 1% blocking buffer (B2), incubated 30 min with anti-digoxigenin-antibody alkaline phosphatase conjugated (750 u/ml, Boehringer Mannheim) diluted 1:15000 in B2, washed in B1 + 0.3% tween 20 (1X 5 min, 1X 15 min, 1X 1 h), equilibrated for 5 min in buffer B3 (0.1 M Tris HCl pH 9.5, 0.1 M NaCl, 50 mM MgCl₂), incubated 45-60 sec in lumigen PPD (Boehringer Mannheim) diluted 1:100 in B3. The humid membrane was sealed in a plastic bag, incubated 15 min at 37°C, and exposed 15 to 20 min to Hyperfilm-ECL (Amersham).
- P_{2x} expression into oocytes** Human urinary bladder P_{2x} cDNA, subcloned into the pBKCMV expression vector, was linearized with NotI, and transcribed in vitro with T3 polymerase in the presence of cap analogue m7G(5')ppp(5')G. Defolliculated *Xenopus* oocytes (Bertrand et al, Electrophysiology of neuronal nicotinic acetylcholine receptors expressed in *Xenopus* oocytes following nuclear injection of genes or cDNAs *Meth Neurosci* 4: 174-193 (1991)) were injected with 50 ng of human P_{2x} in vitro transcribed RNA, and incubated at 18°C for 2-6 days in the ND96 solution (mM): NaCl 96, KCl 2, MgCl₂ 1, CaCl₂ 2, sodium pyruvate 5, HEPES 5, pH 7.6 - 7.5, penicillin (10 U/ml), and streptomycin (10 µg/ml).

Electrophysiology Oocytes were placed in a 1 ml chamber and superfused at 2 - 3 ml/min with ND96 solution with 0.1 mM BaCl₂ replacing the 2 mM CaCl₂ to prevent activation of endogenous calcium-activated chloride currents (Barish, A transient calcium-dependent chloride current in the immature *Xenopus* oocytes *J Physiol* 342: 309-325 (1983)). Currents were measured using a two-electrode voltage-clamp amplifier (Geneclamp Axon Instruments) at a holding potential of -60 mV. Microelectrodes were filled with 3 M KCl (0.5 - 2 MΩ). Data were collected using PClamp software (Axon Instruments). ATP and other purinoceptor agonists were applied by a U-tube perfusion system (Fenwick et al, A patch clamp study of bovine chromaffin cells and their sensitivity to acetylcholine *J Physiol* 331: 577-597 (1982)) placed close (200 - 500 μm) to the oocyte. Initial studies showed that reproducible responses (<10% variation in peak amplitude) could be obtained when ATP (at concentrations up to 1 mM) was applied to hP_{2x} injected oocytes for 5 s every 10 mins. Concentration response relationships to ATP and its analogs were determined by measuring the peak amplitude of responses to a 5 s application of agonist applied at 10 min intervals. Responses to agonists were normalized in each oocyte to the peak response evoked by 100 μM ATP; 100 μM ATP was usually applied at the beginning and at the end of an experiment to determine if there was any rundown of the response. No inward current was recorded in uninjected oocytes in response to application of purinoceptor agonists at the maximal concentration used (n = 3 for each agonist). Antagonists were applied both in the superfusate and together with ATP in the U-tube solution. Antagonists were superfused for 5 - 10 min prior to the application of ATP.

Data analysis Concentration response curves for purinoceptor agonists were fitted with a Hill slope of 1. Equi-effective concentrations i.e. concentration of agonist, giving 50% of the response to 100 μ M ATP, (EEC_{50}) were determined from individual concentration response curves. For antagonists the concentration required to give 50% inhibition (IC_{50}) of the response to 10 μ M ATP (approximately 90% of peak response to ATP) were determined. Data are presented throughout as mean \pm SEM for a given number of oocytes.

Drugs Adenosine, adenosine 5'-monophosphate sodium salt (AMP), adenosine 5'-diphosphate sodium salt (ADP), adenosine 5'-triphosphate magnesium salt (ATP), adenosine 5'-O-(-3-thiophosphate) tetralithium salt (ATP- γ -S), uridine 5'-triphosphate sodium salt (UTP), α,β -methylene ATP lithium salt (α,β -meATP), β,γ -methylene-D-ATP sodium salt (D- β,γ -meATP), 2'-3'-O-(4-benzoylbenzyl)ATP tetraethylammonium salt (BzATP), 4,4'-diisothiocyanatostilbene 2,2'-disulphonic acid, disodium salt (DIDS) were obtained from Sigma. 2-MethylthioATP tetra sodium salt (2MeSATP), 2-chloro-ATP tetra sodium salt, and β - γ -methylene-1-ATP (1- β - γ -meATP) were obtained from RBl. Pyridoxal 5-phosphate monohydrate (Aldrich), p1, p5-di[adenosine-5']pentaphosphate trilithium salt (AP5A) (Boehringer Mannheim), pyridoxal phosphate 6-azophenyl 2',4'-disulphonic acid (PPADS, gift of G. Lambrecht, University of Frankfurt) and suramin (Bayer) were tested. Drugs were prepared from frozen aliquots of stock solutions and diluted to give the required final concentration.

EXAMPLE 6 Sequence and characteristics of hP_{2x} from urinary bladder

Isolation of human P_{2x} cDNA Human urinary bladder tissue
5 was obtained from a cystectomy for a bladder tumor. The
patient showed no symptoms of bladder instability or
urodynamic abnormalities. Only those portions,
surrounding the tumor, which appeared macroscopically
normal (Palea et al - supra) were used. Total RNA was
10 isolated by guanidinium isothiocyanate and poly A⁺ RNA was
purified as described (Valera et al (1994) - supra).
Preparation of a cDNA library in λ gt10, random primer
labelling of a rat smooth muscle P_{2x} probe (Valera et al
(1994) - supra), low stringency hybridisation screening
15 and lambda phage DNA isolation were all done by standard
protocols (Sambrook et al, Molecular Cloning, A
Laboratory Manual, 2nd edn., Cold Spring Harbor
Laboratory Press, New York (1989)). Several independent
phage isolates were examined and the cDNA insert from one
20 was chosen for subcloning into Eco RI-Not I digested
pBKCMTV. This 2677 bp hP_{2x} cDNA was sequenced as described
(Valera et al (1994) - supra).

The 2677 bp cDNA, hP_{2x}, contained a single long open
25 reading frame which corresponds to a protein of 399 amino
acids (Figure 4). This amino acid sequence is highly
homologous with that of the P_{2x} receptor, isolated from
rat vas deferens (89% identity). There are two regions
of hydrophobicity near either end of the protein which
30 are sufficiently long to traverse the membrane but there
is no hydrophobic N-terminal leader sequence. All five
potential sites for glycosylation and all ten cysteine
residues in the central section of the protein are
conserved. In vitro translation of hP_{2x} RNA in the

5 presence of microsomes produced a 60 kD product, whereas translation in the absence of microsomes produced the 45 kD peptide (Figure 6). 45 kD is the computed molecular weight, suggesting that the additional 15 kD results from glycosylation.

10 Some human urinary bladder P_{2x} cDNA was used to transfect HEK293 cells. Stable transfection was confirmed by electrophysiological recording.

EXAMPLE 7 Distribution of human urinary bladder P_{2x} mRNA

15 The distribution of the human urinary bladder P_{2x} mRNA was examined by northern analysis. A single 2.6 kb mRNA species was observed in bladder, placenta, liver and adrenal gland (Figure 8). In thymus, spleen, and lung samples, the 2.6 kb band plus additional higher molecular weight RNAs of 3.6 and 4.2 kb were seen. A smaller additional RNA species of 1.8 kb was observed in spleen and lung. No hybridisation was detected with brain mRNA.

EXAMPLE 8 Induction of hP_{2x} mRNA in HL60 cells

25 A portion of the 3'-untranslated region had been previously deposited in the database (HSGS01701) as an expressed sequence tag for the differentiation of the human promyelocytic cell line, HL60 (Okubo unpublished). We examined the induction of hP_{2x} mRNA in HL60 cells by Northern blot analysis (Figure 7). HL60 cells can be differentiated into distinct lineages, depending on the inductant (Koeffler, Induction of Differentiation of Human Acute Myelogenous Leukemia Cells: Therapeutic Implications *Blood* 62: 709-721 (1983)). Induction of macrophage-like characteristics with phorbol diesters or

30

granulocytic differentiation with DMSO or dibutyl cAMP, each produced an increase in P_{2X} mRNA (Figure 7, lane 6), HL60 RNA (lane 1-5) showed hybridisation of two bands (1.8 and 2.6 kb) and both of these were inducible. This contrasts with the bladder, where Northern analysis showed only a single RNA species (2.6 kb) (Figure 7, lane 6).

EXAMPLE 9 Pharmacological characterization of hP_{2X}

Application of ATP (30 nM - 1mM) to oocytes injected with hP_{2X} receptor RNA evoked inward currents (Figures 9, 10 and 11). Responses to low concentrations of ATP (30 - 300 nM) developed over 3-5 s. Higher concentrations of ATP (1 μ M) evoked responses which peaked within 1 - 1.5 s and then declined during the continued application of ATP (40 - 60% of the peak amplitude after 5 s). The current returned to control values on washout of ATP. The peak amplitude of the inward current evoked by ATP was concentration-dependent (Figures 9, 10 and 11) and could be fitted by a curve with a Hill slope of 1 with a EC_{50} of 0.82 μ M. When ATP (100 μ M) was applied for 5 s every 10 min, reproducible inward currents were recorded. This is in contrast to the responses of the P_{2X} receptor clone from rat vas deferens where a second application of ATP (> 1 μ M) applied 10 mins after the first, evoked an inward current that was ~50% of the initial peak amplitude.

Concentration-response curves were constructed for a number of other P2 purinoceptor agonists (Figures 9, 10 and 11). 2meSATP, 2-chloro-ATP, α,β -meATP and ADP were full agonists. BzATP, AP_5A and ATP- γ -S produced maximal responses of about 65% of the maximal ATP response. The

maximal responses to d and 1- β , γ -meATP were not determined. Adenosine, AMP and UTP (100 μ M) evoked small inward currents (2.3 ± 1.5 , $6.08 \pm .2$, and $3.7 \pm 1.8\%$ of the response to 100 μ M ATP respectively). The EEC₅₀ values and relative potencies of purinoceptor analogs are summarised in Table 1 below.

Table 1

	agonist	EEC50 (μ M)	relative potency
	ATP	0.82	1
	2MeSATP	0.6 ± 0.1	1.36
	2chloroATP	0.76 ± 0.1	1.08
15	AP5A	2 ± 0.2	0.41
	α , β -meATP	3.6 ± 1.6	0.23
	BzATP	4.2 ± 2.2	0.20
	ATP- γ -S	10.6 ± 3.8	0.077
	d, β , γ -meATP	24.1 ± 1.6	0.034
20	ADP	34.3 ± 16	0.024

EEC50: Equi-effective concentrations producing an inward current equivalent to 50% of the peak response to 100 μ M ATP. EEC50 taken from individual fitted concentration response curves with a Hill slope of 1. EEC50 for ATP from mean data from all experiments. (n = 3-4).

EXAMPLE 10 Antagonist studies

The P2-purinoceptor antagonist suramin (1 - 100 μ M) shifted the concentration-response curve for ATP to the right. At 1 μ M suramin the shift was almost parallel. The dissociation equilibrium constant (K_B) estimated from $K_B = 1/(DR-1)$ where DR is the dose ratio was 130 nM. With higher concentrations of suramin the inhibition did not

appear to be competitive. Under the present experimental conditions this K_B estimate is higher than those reported previously for suramin (pA₂ 5.9, Trezise et al, *Br J Pharmacol* 112: 282-288 (1994)) pK_B 5.2, von Kugelgen et al, Interaction of adenine nucleotides, UTP and suramin in mouse vas deferens: suramin-sensitive and suramin-insensitive components in the contractile effect of ATP Naunyn Schmiedeberg's Arch Pharmacol 342: 198-205 (1990)). The antagonism by suramin was fully reversed after 10 mins wash and indicates that the non-competitive antagonism at high concentrations is not due to irreversible binding of the antagonist to the receptor.

The putative P_{2X} purinoceptor antagonists PPADS, DIDS and pyridoxal 5 phosphate (Ziganshin et al, Selective antagonism by PPADS at P_{2X} purinoceptors in rabbit isolated blood vessels *Br J Pharmacol* 111: 923-929 (1994), Bultmann & Starke, Blockade by 4,4'-diisothiocyanatostilben-2,2'-disulphonate (DIDS) of P_{2X} purinoceptors in rat vas deferens *Br J Pharmacol* 112: 690-694 (1994), Trezise et al, *Eur J Pharmacol* 259: 295-300 (1994)) inhibited inward currents evoked by 10 μ M ATP (approximately EC₉₀ concentration) in a concentration dependent manner (Figures 12 and 13). Suramin PPADS and DIDS were equally effective in inhibiting ATP evoked currents (IC₅₀ ~ 1 μ M). The IC 50 for P5P was ~ 20 μ M. PPADS and P5P antagonism was readily reversible on washout. In contrast, inhibitory effects of DIDS (100 μ M) were very slow to reverse on washout.

(iii) RAT SUPERIOR CERVICAL GANGLION P_{2X} RECEPTOR

Example 11 Isolation and functional expression of a cDNA encoding a P_{2X} receptor from rat superior cervical ganglion (referred to herein as clone 3)

A 440 bp fragment was amplified by polymerase chainreaction (PCR) from rat testis cDNA, using degenerate primers based on conserved nucleotide sequences within the rat vas deferens P_{2X} receptor cDNA and on the sequence of PC12 cDNA (Ehrlich H A (ed) PCR Technology MacMillan, Basingstoke (1989)). The primers used are given below:

15

Sense

5' T G T/C G A A/G A/G T I T T/C I G G/C I T G G T G
T/C C C 3' (SEQ ID NO 2)

20

Antisense

5' G C A/G A A T/C C T A/G A A A/G T T A/G T/A A
I C C 3' (SEQ ID NO 3)

25

(wherein I = Inosine and "T/C" indicates that either T or C is present at the position indicated (this applies *mutatis mutandis* to the other alternatives given).

30

The cloned PCR fragment was labelled and used as a hybridization probe for screening a rat testis cDNA bank in λZAP. One recombinant phage was positive, and its insert was excised and transferred to a plasmid (#432). This cDNA was 1500 bp with a single EcoR1 site (at position 1000, still in the open reading frame). The 5' end of the cDNA was too short to encode the entire N terminus.

35

Internal primers specific to the new sequence were made and the tissue distribution was tested by PCR. The candidate was present in mRNA prepared from phaeochromocytoma (PC12) cells, intestine and superior cervical ganglion (scg). The hybridization probe was therefore used to screen a rat scg cDNA bank in λ gt10. From 30 initial positives, 20 pure phage DNA stocks were prepared; 19 were various portions of the candidate sequence, and the insert from one was transferred to plasmid (p457) and sequenced. The insert appeared to be a full length cDNA; it has a single open reading frame of 388 amino acids (Fig. 2). The insert from p457 was subcloned into pcDNA3 (p464) and used to transfect human embryonic kidney (HEK293) cells.

The functional characterisation of the clone illustrated in Fig 2 (referred to herein as clone 3) was carried out by electrical recordings from transfected HEK293 cells and from oocytes injected with the *in vitro* transcribed RNA, as described in Example 4 for the rat vas deferens P_{2X} receptor. Table A summarizes the main properties of clone 3 as compared to those of rat vas/human bladder cDNA clone, and the PC12 cDNA clone (provided by David Julius and Tony Brake of the University of California at San Francisco).

TABLE A
Functional Properties of 3 cloned P_{2X} Receptors

5	kinetics	bladder	clone 3	PC12	
	desensitization	very strong	very little	very little	
	rundown	profound	very little	very little	
10	ionic permeability				
	monovalent	no differences	no differences	no differences	
	divalent (Ca ⁺⁺)	high permeability	high permeability	high permeability	
	Ca ⁺⁺ block	none	intermediate	very strong	
15	agonist profile				
	ATP	0.7 μ M	11 μ M	8 μ M	
	α, β -meATP	3 μ M	>>100 mM	>>100 μ M	
20	antagonist profile				
	suramin	1 μ M	< 40% block	6 μ M	
	PPADS	1 μ M	< 30% block	1 μ M	
	P-5-P	6 μ M	< 40% block	6 μ M	
	DIDS	1 μ M		> 100 μ M	

The main functional properties of clone 3 are as follows.

- (a) The currents evoked by ATP show little or no decline during applications of several seconds; that is, there is little desensitisation (Fig. 14). (b) The relative permeabilities of the ionic pore to sodium, potassium, cesium, tetraethylammonium and to calcium are not different to those observed for the rat vas deferens/human bladder or the PC12 forms of the receptor.
- 5 (c) Extracellular calcium (30 mM) inhibits the inward current through the P_{2X} receptor channel of the PC12 form whereas it does not block current through the rat vas deferens/human bladder form; clone 3 is intermediate in sensitivity. (d) The effectiveness of agonists that are structurally related to ATP is the same as that found for
- 10 the PC12 form; most notably, $\alpha\beta$ methylene ATP has little or no agonist action (Fig. 14). (e) Currents activated by ATP at the clone 3 receptor were much less sensitive to antagonism by suramin., pyridoxal 5'-phosphate and pyridoxal-6-azophenyl-2',4'-disulphonic acid (PPADS) than
- 15 were similar current mediated by the other two forms (rat vas deferens/human bladder; PC12) (Fig. 15).
- 20

(iv) RAT DORSAL ROOT GANGLION P_{2X} RECEPTOR

Example 12 Isolation of a cDNA encoding a P_{2X} receptor from a rat dorsal root ganglion

5

By using PCR with the same primers as used in Example 11 above, but using different cDNA sources, further P_{2X} family members can be found.

10

Using this method, rat dorsal root ganglion P_{2X} receptor cDNA was isolated. Fig. 1B shows the cDNA sequence of this clone (referred to herein as clone 6), together with the putative amino acid sequence. The portions underlined in this figure correspond to the PCR primers initially used.

15

A similar procedure to that described in Example 11 was then used to isolate the full length cDNA.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: GLAXO GROUP LIMITED
- (B) STREET: GLAXO HOUSE, BERKELEY AVENUE
- (C) CITY: GREENFORD
- (D) STATE: MIDDLESEX
- (E) COUNTRY: UNITED KINGDOM
- (F) POSTAL CODE (ZIP): UB6 0NN

(ii) TITLE OF INVENTION: DNA AND PROTEIN SEQUENCES

(iii) NUMBER OF SEQUENCES: 11

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAGAGAGAGA GCGGCCGCTT TTTTTTTTTT TTT

33

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:3
 (D) OTHER INFORMATION:/mod_base= OTHER
 /note= "T or C"
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:6
 (D) OTHER INFORMATION:/mod_base= OTHER
 /note= "A or G"
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:7
 (D) OTHER INFORMATION:/mod_base= OTHER
 /note= "A or G"
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:9
 (D) OTHER INFORMATION:/mod_base= 1
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:11
 (D) OTHER INFORMATION:/mod_base= OTHER
 /note= "T or C"
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:12
 (D) OTHER INFORMATION:/mod_base= i
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:14
 (D) OTHER INFORMATION:/mod_base= OTHER
 /note= "G or C"
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:15
 (D) OTHER INFORMATION:/mod_base= i
- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION:21
 (D) OTHER INFORMATION:/mod_base= OTHER
 /note= "T or C"

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TGNGANNNTNT NNGNNTGGTG NCC

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:3
 - (D) OTHER INFORMATION:/mod_base= OTHER
/note= "A or G"

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:6
 - (D) OTHER INFORMATION:/mod_base= OTHER
/note= "T or C"

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/mod_base= OTHER
/note= "A or G"

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/mod_base= OTHER
/note= "A or G"

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:15
 - (D) OTHER INFORMATION:/mod_base= OTHER
/note= "A or G"

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:16
 - (D) OTHER INFORMATION:/mod_base= OTHER
/note= "T or A"

- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCNAANCTNA ANTNNANCC

(2) INFORMATION FOR SEQ ID NO: 4:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1837 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rat P2x from vas deferens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 210..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCCAAAAGCT GTTCTGATCA CCCAGGGTTT TTCCTCCCAA CCCAGACCCC ACCATCGAAC	60
CTCCAACCTCT GGTCCACCT AGCCTGCTCT GTCCTTAAGG GGCCGGGAAG CCCAGTCAC	120
TCCACTGCTA TTGTAGATGC AGATGGTGGC CTGCCCTTGA CCATAGAGGC CGTGTGGGGT	180
GTTCATCTCT GAGCCCCTTC TGGCCACC ATG GCT CGG CGG CTG CAA GAT GAG	233
Met Ala Arg Arg Leu Gln Asp Glu	
1 5	
CTG TCA GCC TTC TTC TTT GAA TAT GAC ACT CCC CGG ATG GTG CTG GTA	281
Leu Ser Ala Phe Phe Phe Glu Tyr Asp Thr Pro Arg Met Val Leu Val	
10 15 20	
CGA AAC AAG AAG GTG GGA GTC ATT TTC CGT CTG ATC CAG TTG GTG GTT	329
Arg Asn Lys Lys Val Gly Val Ile Phe Arg Leu Ile Gln Leu Val Val	
25 30 35 40	
CTG GTC TAC GTC ATT GGG TGG GTG TTT GTC TAT GAA AAA GGA TAC CAG	377
Leu Val Tyr Val Ile Gly Trp Val Phe Val Tyr Glu Lys Gly Tyr Gln	
45 50 55	
ACC TCA AGT GAC CTC ATC AGC AGT GTG TCC GTG AAG CTC AAG GGC TTG	425
Thr Ser Ser Asp Leu Ile Ser Ser Val Ser Val Lys Leu Lys Gly Leu	
60 65 70	
GCT GTG ACC CAG CTC CAG GGC CTG GGA CCC CAG GTC TGG GAC GTG GCT	473
Ala Val Thr Gln Leu Gln Gly Leu Gly Pro Gln Val Trp Asp Val Ala	
75 80 85	
GAC TAT GTC TTC CCA GCA CAC GGG GAC AGC TCC TTT GTA GTT ATG ACC	521
Asp Tyr Val Phe Pro Ala His Gly Asp Ser Ser Phe Val Val Met Thr	
90 95 100	
AAC TTC ATC GTG ACC CCT CAG CAG ACT CAA GGC CAT TGT GCA GAG AAC	569
Asn Phe Ile Val Thr Pro Gln Gln Thr Gln Gly His Cys Ala Glu Asn	
105 110 115 120	

CCA GAA GGT GGC ATA TGC CAG GAT GAC AGT GGC TGC ACT CCA GGA AAA Pro Glu Gly Gly Ile Cys Gln Asp Asp Ser Gly Cys Thr Pro Gly Lys 125 130 135	617
GCA GAA AGG AAA GCC CAA GGT ATT CGC ACA GGC AAC TGT GTG CCC TTC Ala Glu Arg Lys Ala Gln Gly Ile Arg Thr Gly Asn Cys Val Pro Phe 140 145 150	665
AAT GGC ACT GTG AAG ACA TGT GAG ATC TTT GGT TGG TGT CCT GTA GAG Asn Gly Thr Val Lys Thr Cys Glu Ile Phe Gly Trp Cys Pro Val Glu 155 160 165	713
GTG GAT GAC AAG ATC CCA AGC CCT GCT CTT CTT CGT GAG GCT GAG AAC Val Asp Asp Lys Ile Pro Ser Pro Ala Leu Leu Arg Glu Ala Glu Asn 170 175 180	761
TTC ACC CTC TTC ATC AAA AAC AGC ATC AGC TTT CCA CGC TTC AAG GTC Phe Thr Leu Phe Ile Lys Asn Ser Ile Ser Phe Pro Arg Phe Lys Val 185 190 195 200	809
AAC AGG CGC AAC CTG GTA GAG GAG GTG AAC GGC ACC TAC ATG AAG AAG Asn Arg Arg Asn Leu Val Glu Glu Val Asn Gly Thr Tyr Met Lys Lys 205 210 215	857
TGC CTC TAT CAC AAG ATT CAA CAC CCC CTG TGC CCA GTC TTC AAC CTT Cys Leu Tyr His Lys Ile Gln His Pro Leu Cys Pro Val Phe Asn Leu 220 225 230	905
GGC TAT GTG GTG CGA GAG TCA GGC CAG GAC TTC CGC AGC CTT GCT GAG Gly Tyr Val Val Arg Glu Ser Gly Gln Asp Phe Arg Ser Leu Ala Glu 235 240 245	953
AAG GGT GGG GTG GTT GGT ATC ACC ATT GAC TGG AAG TGT GAT CTG GAC Lys Gly Gly Val Val Gly Ile Thr Ile Asp Trp Lys Cys Asp Leu Asp 250 255 260	1001
TGG CAC GTT CGG CAC TGC AAA CCC ATC TAC CAG TTC CAC GGA CTG TAT Trp His Val Arg His Cys Lys Pro Ile Tyr Gln Phe His Gly Leu Tyr 265 270 275 280	1049
GGG GAG AAG AAC CTG TCT CCA GGC TTC AAC TTC AGA TTT GCC AGG CAT Gly Glu Lys Asn Leu Ser Pro Gly Phe Asn Phe Arg Phe Ala Arg His 285 290 295	1097
TTC GTG CAG AAT GGG ACA AAC CGT CGT CAC CTC TTC AAG GTG TTT GGG Phe Val Gln Asn Gly Thr Asn Arg Arg His Leu Phe Lys Val Phe Gly 300 305 310	1145
ATT CAC TTT GAT ATC CTT GTG GAT GGC AAG GCT GGG AAG TTT GAC ATC Ile His Phe Asp Ile Leu Val Asp Gly Lys Ala Gly Lys Phe Asp Ile 315 320 325	1193
ATC CCT ACT ATG ACT ACT ATC GGT TCT GGG ATT GGC ATC TTT GGA GTG Ile Pro Thr Met Thr Thr Ile Gly Ser Gly Ile Gly Ile Phe Gly Val 330 335 340	1241
GCC ACA GTG CTT TGT GAT CTC TTA TTG CTC CAC ATC CTG CCT AAG AGG Ala Thr Val Leu Cys Asp Leu Leu Leu Leu His Ile Leu Pro Lys Arg 345 350 355 360	1289

CAC TAC TAC AAG CAG AAG AAG TTC AAA TAT GCC GAG GAC ATG GGG CCG His Tyr Tyr Lys Gln Lys Lys Phe Lys Tyr Ala Glu Asp Met Gly Pro 365 370 375	1337
GGA GAG GGT GAA CAT GAC CCC GTG GCC ACC AGC TCC ACT CTG GGC CTG Gly Glu Gly Glu His Asp Pro Val Ala Thr Ser Ser Thr Leu Gly Leu 380 385 390	1385
CAG GAG AAC ATG AGG ACC TCC TGACCTTAGT CTTGAGATCC GGACTTGACG Gln Glu Asn Met Arg Thr Ser 395	1436
CAGTGTGTGG CTTCCGGCAA GGGCTGATGG CTTTGAGCCA GGGCAGAGGG CATTCCCAGA	1496
GGCTTTCCTG CAAGGCAGAC ACCAGTGGCC CTCTGGTTCA GCATGAAGAC AGGCAAGACT	1556
TTGGATTTCA GAGCTCTGGT TTCAGTTCCA CATGTCCCTT CCTGAGGGAT GCCTCCTCCA	1616
GTTTTCACCA ATTTGGGTTC ATATGGCTGG GCCCCTCACA CATCTATACT CTAGCTTTGT	1676
GCTTAAGGCT CAGGCTGTCA TTGTCTTTCC CACAGCCTTA CCTGCCTAGA TTTGGGCTCT	1736
TCCACATGGT AGCCACTAGC CAGATGTGTC AGTTTGAAC TTAATTAATAA TATAATAAAA	1796
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	1837

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

Met Ala Arg Arg Leu Gln Asp Glu Leu Ser Ala Phe Phe Phe Glu Tyr
 1           5           10           15
Asp Thr Pro Arg Met Val Leu Val Arg Asn Lys Lys Val Gly Val Ile
      20           25           30
Phe Arg Leu Ile Gln Leu Val Val Leu Val Tyr Val Ile Gly Trp Val
      35           40           45
Phe Val Tyr Glu Lys Gly Tyr Gln Thr Ser Ser Asp Leu Ile Ser Ser
      50           55           60
Val Ser Val Lys Leu Lys Gly Leu Ala Val Thr Gln Leu Gln Gly Leu
      65           70           75           80
Gly Pro Gln Val Trp Asp Val Ala Asp Tyr Val Phe Pro Ala His Gly
      85           90           95
Asp Ser Ser Phe Val Val Met Thr Asn Phe Ile Val Thr Pro Gln Gln
      100          105          110
Thr Gln Gly His Cys Ala Glu Asn Pro Glu Gly Gly Ile Cys Gln Asp
      115          120          125
Asp Ser Gly Cys Thr Pro Gly Lys Ala Glu Arg Lys Ala Gln Gly Ile
      130          135          140
Arg Thr Gly Asn Cys Val Pro Phe Asn Gly Thr Val Lys Thr Cys Glu
      145          150          155          160
Ile Phe Gly Trp Cys Pro Val Glu Val Asp Asp Lys Ile Pro Ser Pro
      165          170          175
Ala Leu Leu Arg Glu Ala Glu Asn Phe Thr Leu Phe Ile Lys Asn Ser
      180          185          190
Ile Ser Phe Pro Arg Phe Lys Val Asn Arg Arg Asn Leu Val Glu Glu
      195          200          205
Val Asn Gly Thr Tyr Met Lys Lys Cys Leu Tyr His Lys Ile Gln His
      210          215          220
Pro Leu Cys Pro Val Phe Asn Leu Gly Tyr Val Val Arg Glu Ser Gly
      225          230          235          240
Gln Asp Phe Arg Ser Leu Ala Glu Lys Gly Gly Val Val Gly Ile Thr
      245          250          255
Ile Asp Trp Lys Cys Asp Leu Asp Trp His Val Arg His Cys Lys Pro
      260          265          270

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Ile Tyr Gln Phe His Gly Leu Tyr Gly Glu Lys Asn Leu Ser Pro Gly
 275 280 285
 Phe Asn Phe Arg Phe Ala Arg His Phe Val Gln Asn Gly Thr Asn Arg
 290 295 300
 Arg His Leu Phe Lys Val Phe Gly Ile His Phe Asp Ile Leu Val Asp
 305 310 315 320
 Gly Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met Thr Thr Ile Gly
 325 330 335
 Ser Gly Ile Gly Ile Phe Gly Val Ala Thr Val Leu Cys Asp Leu Leu
 340 345 350
 Leu Leu His Ile Leu Pro Lys Arg His Tyr Tyr Lys Gln Lys Lys Phe
 355 360 365
 Lys Tyr Ala Glu Asp Met Gly Pro Gly Glu Gly Glu His Asp Pro Val
 370 375 380
 Ala Thr Ser Ser Thr Leu Gly Leu Gln Glu Asn Met Arg Thr Ser
 385 390 395

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1997 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rat P2x clone 3

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:101..1264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CGCAGCGAGC CTGCCGGAGC TGGTGGGTGG AGCTACGACC GGGAGCCGAC GGTGGCGAGG	60
GGACCCACAG TGTCCAAGGC GCGGAGCGGT CGGCGGAGCC ATG GCG GGC TGC TGC	115
Met Ala Gly Cys Cys	
400	
TCC GTG CTC GGG TCC TTC CTG TTC GAG TAC GAC ACG CCG CGC ATC GTG	163
Ser Val Leu Gly Ser Phe Leu Phe Glu Tyr Asp Thr Pro Arg Ile Val	
405 410 415 420	
CTC ATC CGC AGC CGT AAA GTG GGG CTC ATG AAC CGC GCG GTG CAG CTG	211
Leu Ile Arg Ser Arg Lys Val Gly Leu Met Asn Arg Ala Val Gln Leu	
425 430 435	
CTC ATC CTG GCT TAC GTC ATC GGG TGG GTG TTC GTG TGG GAA AAG GGC	259
Leu Ile Leu Ala Tyr Val Ile Gly Trp Val Phe Val Trp Glu Lys Gly	
440 445 450	
TAC CAG GAA ACG GAC TCC GTG GTC AGC TCG GTG ACA ACC AAA GCC AAA	307
Tyr Gln Glu Thr Asp Ser Val Val Ser Ser Val Thr Thr Lys Ala Lys	
455 460 465	
GGT GTG GCT GTG ACC AAC ACC TCT CAG CTT GGA TTC CGG ATC TGG GAC	355
Gly Val Ala Val Thr Asn Thr Ser Gln Leu Gly Phe Arg Ile Trp Asp	
470 475 480	
GTG GCG GAC TAT GTG ATT CCA GCT CAG GAG GAA AAC TCC CTC TTC ATT	403
Val Ala Asp Tyr Val Ile Pro Ala Gln Glu Glu Asn Ser Leu Phe Ile	
485 490 495 500	
ATG ACC AAC ATG ATT GTC ACC GTG AAC CAG ACA CAG AGC ACC TGT CCA	451
Met Thr Asn Met Ile Val Thr Val Asn Gln Thr Gln Ser Thr Cys Pro	
505 510 515	
GAG ATT CCT GAT AAG ACC AGC ATT TGT AAT TCA GAC GCC GAC TGC ACT	499
Glu Ile Pro Asp Lys Thr Ser Ile Cys Asn Ser Asp Ala Asp Cys Thr	
520 525 530	

CCT GGC TCC GTG GAC ACC CAC AGC AGT GGA GTT GCG ACT GGA AGA TGT Pro Gly Ser Val Asp Thr His Ser Ser Gly Val Ala Thr Gly Arg Cys 535 540 545	547
GTT CCT TTC AAT GAG TCT GTG AAG ACC TGT GAG GTG GCT GCA TGG TGC Val Pro Phe Asn Glu Ser Val Lys Thr Cys Glu Val Ala Ala Trp Cys 550 555 560	595
CCG GTG GAG AAC GAC GTT GGC GTG CCA ACG CCG GCT TTC TTA AAG GCT Pro Val Glu Asn Asp Val Gly Val Pro Thr Pro Ala Phe Leu Lys Ala 565 570 575 580	643
GCA GAA AAC TTC ACC CTC TTG GTA AAG AAC AAC ATC TGG TAC CCC AAG Ala Glu Asn Phe Thr Leu Leu Val Lys Asn Asn Ile Trp Tyr Pro Lys 585 590 595	691
TTT AAC TTC AGC AAG AGG AAC ATC CTC CCC AAC ATC ACC ACG TCC TAC Phe Asn Phe Ser Lys Arg Asn Ile Leu Pro Asn Ile Thr Thr Ser Tyr 600 605 610	739
CTC AAA TCG TGC ATT TAC AAT GCT CAA ACG GAT CCC TTC TGC CCC ATA Leu Lys Ser Cys Ile Tyr Asn Ala Gln Thr Asp Pro Phe Cys Pro Ile 615 620 625	787
TTC CGT CTT GGC ACA ATC GTG GGG GAC GCG GGA CAT AGC TTC CAG GAG Phe Arg Leu Gly Thr Ile Val Gly Asp Ala Gly His Ser Phe Gln Glu 630 635 640	835
ATG GCA GTT GAG GGA GGC ATC ATG GGT ATC CAG ATC AAG TGG GAC TGC Met Ala Val Glu Gly Gly Ile Met Gly Ile Gln Ile Lys Trp Asp Cys 645 650 655 660	883
AAC CTG GAT AGA GCC GCC TCC CTT TGC CTG CCC AGA TAT TCC TTC CGG Asn Leu Asp Arg Ala Ala Ser Leu Cys Leu Pro Arg Tyr Ser Phe Arg 665 670 675	931
CGC CTG GAC ACC CGG GAC CTG GAA CAC AAT GTG TCT CCT GGC TAC AAT Arg Leu Asp Thr Arg Asp Leu Glu His Asn Val Ser Pro Gly Tyr Asn 680 685 690	979
TTC AGG TTT GCC AAG TAC TAC AGG GAC CTG GCC GGC AAA GAG CAG CGC Phe Arg Phe Ala Lys Tyr Tyr Arg Asp Leu Ala Gly Lys Glu Gln Arg 695 700 705	1027
ACA CTC ACC AAG GCG TAC GGC ATC CGC TTT GAC ATC ATC GTG TTT GGA Thr Leu Thr Lys Ala Tyr Gly Ile Arg Phe Asp Ile Ile Val Phe Gly 710 715 720	1075
AAG GCT GGG AAG TTT GAC ATC ATC CCT ACC ATG ATC AAC GTT GGC TCT Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met Ile Asn Val Gly Ser 725 730 735 740	1123
GGC TTG GCG CTC CTC GGG GTG GCG ACG GTG CTC TGT GAC GTC ATA GTC Gly Leu Ala Leu Leu Gly Val Ala Thr Val Leu Cys Asp Val Ile Val 745 750 755	1171
CTC TAC TGC ATG AAG AAG AAA TAC TAC TAC CGG GAC AAG AAA TAT AAG Leu Tyr Cys Met Lys Lys Lys Tyr Tyr Tyr Arg Asp Lys Lys Tyr Lys 760 765 770	1219

TAT GTG GAA GAC TAC GAG CAG GGT CTT TCG GGG GAG ATG AAC CAG	1264
Tyr Val Glu Asp Tyr Glu Gln Gly Leu Ser Gly Glu Met Asn Gln	
775 780 785	
TGACGCCTAA AGTTACATTT CCACCCCGCT CAGCCCGCGA AGCAGAAAGA TGGGGAGAGA	1324
TGGCTACTGC GTCTGTCACT CTAGAGAAAG CTCCAGAGTT TCAGCTCAGT TCTCCACTCC	1384
ACAAATACTC AGGGTTGCCA AGCACATCTT GTTGGAGCCC GGCTCTTGCT CTGCTGCTCA	1444
GATGGGCTTC CAGATACAAG AATCCTCCTG CTTCTGCCTC TAGGAATGCT GGGATCAAAC	1504
ATGTCACTTG CAATGCCCAT TTCCCATGGG GAGTTTGGCA TTTTITACAT TTTACCCTTT	1564
CCTTTTGTAT ACATCTAAGG CTGCCCTCAG ACGCAAGACG TTCTTCCACC CTATACACCC	1624
TTTAAATCTC ACTGTGTGTG GGAGGGGGGT CGTTTGCACA CGACGCACGG TGGATGTCTG	1684
GTGTGCTGTT GGCTGGGCCA CCTGTGGCTT ATACAGTGTG AGCGTATGGA GGTAGGAAGG	1744
GTCTGAGAGC AGAGACACTG CTGTGGCTTA CGGACAGGCC CAGGCTCTGT CCACGCACTT	1804
TATTTCTAAG GAAGGAGGCT CTCTCAGGTG CTGTCAGCAG GCCTGGGACA CCATTCCTCT	1864
TCCCTATAAT CAGAGAAGTT GTCCTGTAG CAAAGGCAGG GTTAGCTTTT CCTTTTATAA	1924
GGGCTGTGTT GAAATGACCT AGGACCAAAC ATTAAGAGAA ATAATTTTTT AAAAAAAAAA	1984
AAAAAAAAA AAA	1997

(2) INFORMATION FOR SEQ ID NO: 7:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Gly Cys Cys Ser Val Leu Gly Ser Phe Leu Phe Glu Tyr Asp
 1 5 10 15
 Thr Pro Arg Ile Val Leu Ile Arg Ser Arg Lys Val Gly Leu Met Asn
 20 25 30
 Arg Ala Val Gln Leu Leu Ile Leu Ala Tyr Val Ile Gly Trp Val Phe
 35 40 45
 Val Trp Glu Lys Gly Tyr Gln Glu Thr Asp Ser Val Val Ser Ser Val
 50 55 60
 Thr Thr Lys Ala Lys Gly Val Ala Val Thr Asn Thr Ser Gln Leu Gly
 65 70 75 80
 Phe Arg Ile Trp Asp Val Ala Asp Tyr Val Ile Pro Ala Gln Glu Glu
 85 90 95
 Asn Ser Leu Phe Ile Met Thr Asn Met Ile Val Thr Val Asn Gln Thr
 100 105 110
 Gln Ser Thr Cys Pro Glu Ile Pro Asp Lys Thr Ser Ile Cys Asn Ser
 115 120 125
 Asp Ala Asp Cys Thr Pro Gly Ser Val Asp Thr His Ser Ser Gly Val
 130 135 140
 Ala Thr Gly Arg Cys Val Pro Phe Asn Glu Ser Val Lys Thr Cys Glu
 145 150 155 160
 Val Ala Ala Trp Cys Pro Val Glu Asn Asp Val Gly Val Pro Thr Pro
 165 170 175
 Ala Phe Leu Lys Ala Ala Glu Asn Phe Thr Leu Leu Val Lys Asn Asn
 180 185 190
 Ile Trp Tyr Pro Lys Phe Asn Phe Ser Lys Arg Asn Ile Leu Pro Asn
 195 200 205
 Ile Thr Thr Ser Tyr Leu Lys Ser Cys Ile Tyr Asn Ala Gln Thr Asp
 210 215 220
 Pro Phe Cys Pro Ile Phe Arg Leu Gly Thr Ile Val Gly Asp Ala Gly
 225 230 235 240
 His Ser Phe Gln Glu Met Ala Val Glu Gly Gly Ile Met Gly Ile Gln
 245 250 255
 Ile Lys Trp Asp Cys Asn Leu Asp Arg Ala Ala Ser Leu Cys Leu Pro
 260 265 270

Arg Tyr Ser Phe Arg Arg Leu Asp Thr Arg Asp Leu Glu His Asn Val
 275 280 285
 Ser Pro Gly Tyr Asn Phe Arg Phe Ala Lys Tyr Tyr Arg Asp Leu Ala
 290 295 300
 Gly Lys Glu Gln Arg Thr Leu Thr Lys Ala Tyr Gly Ile Arg Phe Asp
 305 310 315 320
 Ile Ile Val Phe Gly Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met
 325 330 335
 Ile Asn Val Gly Ser Gly Leu Ala Leu Leu Gly Val Ala Thr Val Leu
 340 345 350
 Cys Asp Val Ile Val Leu Tyr Cys Met Lys Lys Lys Tyr Tyr Tyr Arg
 355 360 365
 Asp Lys Lys Tyr Lys Tyr Val Glu Asp Tyr Glu Gln Gly Leu Ser Gly
 370 375 380
 Glu Met Asn Gln
 385

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rat P2x clone 6

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 163..1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CACTGGGCTA CAGTTGCCTG GCTTACAGGA ACTGGCTCTT TTCCTCAAGC CTCATTAAGC	60
AGCCCACTCC AGTTCTTGAT CTTTGTCTCC CAGTCCTGAA GTCCTTTCTC TCCTTAGGCT	120
GCATCCACAG CCCTTCTAAG TGGCTGTGAG CAGTTTCTCA GT ATG AAC TGT ATA	174
Met Asn Cys Ile	
390	
TCA GAC TTC TTC ACC TAC GAG ACT ACC AAG TCG GTG GTT GTG AAG AGC	222
Ser Asp Phe Phe Thr Tyr Glu Thr Thr Lys Ser Val Val Val Lys Ser	
395 400 405	
TGG ACC ATT GGG ATC ATC AAC CGA GCC GTC CAG CTG CTG ATT ATC TCC	270
Trp Thr Ile Gly Ile Ile Asn Arg Ala Val Gln Leu Leu Ile Ile Ser	
410 415 420	
TAC TTT GTG GGG TGG GTT TTC TTG CAT GAG AAG GCC TAC CAA GTG AGG	318
Tyr Phe Val Gly Trp Val Phe Leu His Glu Lys Ala Tyr Gln Val Arg	
425 430 435 440	
GAC ACC GCC ATT GAG TCC TCA GTA GTT ACA AAG GTG AAA GGC TTC GGG	366
Asp Thr Ala Ile Glu Ser Ser Val Val Thr Lys Val Lys Gly Phe Gly	
445 450 455	
CGC TAT GCC AAC AGA GTC ATG GAC GTG TCG GAT TAT GTG ACC CCA CCC	414
Arg Tyr Ala Asn Arg Val Met Asp Val Ser Asp Tyr Val Thr Pro Pro	
460 465 470	
CAG GGC ACC TCT GTC TTT GTC ATC ATC ACC AAA ATG ATC GTT ACT GAA	462
Gln Gly Thr Ser Val Phe Val Ile Ile Thr Lys Met Ile Val Thr Glu	
475 480 485	
AAT CAA ATG CAA GGA TTC TGT CCA GAG AAT GAA GAG AAG TAC CGC TGT	510
Asn Gln Met Gln Gly Phe Cys Pro Glu Asn Glu Glu Lys Tyr Arg Cys	
490 495 500	
GTG TCT GAC AGC CAG TGT GGG CCT GAA CGC TTC CCA GGT GGG GGG ATC	558
Val Ser Asp Ser Gln Cys Gly Pro Glu Arg Phe Pro Gly Gly Gly Ile	
505 510 515 520	

CTC ACC GGC CGC TGC GTG AAC TAC AGC TCT GTT CTC CGG ACC TGT GAG Leu Thr Gly Arg Cys Val Asn Tyr Ser Ser Val Leu Arg Thr Cys Glu 525 530 535	606
ATC CAG GGC TGG TGC CCC ACT GAG GTG GAC ACC GTG GAG ATG CCT ATC Ile Gln Gly Trp Cys Pro Thr Glu Val Asp Thr Val Glu Met Pro Ile 540 545 550	654
ATG ATG GAG GCT GAG AAC TTC ACC ATT TTC ATC AAG AAC AGC ATC CGT Met Met Glu Ala Glu Asn Phe Thr Ile Phe Ile Lys Asn Ser Ile Arg 555 560 565	702
TTC CCT CTC TTC AAC TTT GAG AAG GGA AAC CTC CTG CCT AAC CTC ACC Phe Pro Leu Phe Asn Phe Glu Lys Gly Asn Leu Leu Pro Asn Leu Thr 570 575 580	750
GAC AAG GAC ATA AAG AGG TGC CGC TTC CAC CCT GAA AAG GCC CCA TTT Asp Lys Asp Ile Lys Arg Cys Arg Phe His Pro Glu Lys Ala Pro Phe 585 590 595 600	798
TGC CCC ATC TTG AGG GTA GGG GAT GTG GTT AAG TTT GCT GGA CAG GAT Cys Pro Ile Leu Arg Val Gly Asp Val Val Lys Phe Ala Gly Gln Asp 605 610 615	846
TTT GCC AAG CTG GCC CGC ACG GGT GGC GTT CTG GGT ATT AAG ATC GGC Phe Ala Lys Leu Ala Arg Thr Gly Gly Val Leu Gly Ile Lys Ile Gly 620 625 630	894
TGG GTG TGC GAT CTA GAC AAG GCC TGG GAC CAG TGC ATC CCT AAA TAT Trp Val Cys Asp Leu Asp Lys Ala Trp Asp Gln Cys Ile Pro Lys Tyr 635 640 645	942
TCC TTC ACT CGG CTG GAT GGA GTT TCT GAG AAA AGC AGT GTT TCC CCT Ser Phe Thr Arg Leu Asp Gly Val Ser Glu Lys Ser Ser Val Ser Pro 650 655 660	990
GGC TAC AAC TTC AGG TTT GCC AAA TAC TAT AAG ATG GAG AAC GGC AGC Gly Tyr Asn Phe Arg Phe Ala Lys Tyr Tyr Lys Met Glu Asn Gly Ser 665 670 675 680	1038
GAG TAC CGC ACA CTC CTG AAG GCT TTT GGC ATC CGC TTT GAT GTG CTG Glu Tyr Arg Thr Leu Leu Lys Ala Phe Gly Ile Arg Phe Asp Val Leu 685 690 695	1086
GTA TAT GGG AAC GCT GGC AAG TTC AAC ATC ATC CCC ACC ATT ATC AGC Val Tyr Gly Asn Ala Gly Lys Phe Asn Ile Ile Pro Thr Ile Ile Ser 700 705 710	1134
TCG GTG GCG GCC TTC ACT TCT GTG GGA GTG GGC ACT GTT CTC TGT GAC Ser Val Ala Ala Phe Thr Ser Val Gly Val Gly Thr Val Leu Cys Asp 715 720 725	1182
ATC ATC CTG CTC AAT TTC CTC AAA GGG GCT GAT CAC TAC AAA GCC AGG Ile Ile Leu Leu Asn Phe Leu Lys Gly Ala Asp His Tyr Lys Ala Arg 730 735 740	1230
AAG TTT GAG GAG GTG ACT GAG ACA ACA CTG AAG GGT ACT GCG TCA ACC Lys Phe Glu Glu Val Thr Glu Thr Thr Leu Lys Gly Thr Ala Ser Thr 745 750 755 760	1278

AAC CCA GTG TTC GCC AGT GAC CAG GCC ACT GTG GAG AAG CAG TCT ACA	1326
Asn Pro Val Phe Ala Ser Asp Gln Ala Thr Val Glu Lys Gln Ser Thr	
765 770 775	
GAC TCA GGG GCC TAT TCT ATT GGT CAC TAGGGCCTCT TCCCAGGGTT	1373
Asp Ser Gly Ala Tyr Ser Ile Gly His	
780 785	
CCATGCTCAC CCTTAGGCTG CAGAACCTGC AACAGGCCA CTCTATCTAA GCAGTCAGGG	1433
GTGGGAGGGG GAGAAGAAGG GCTGCTATTT CTGCTGTTCA CCCCAGAGAC TAGATCCAGA	1493
TATCTAGGCC CTCAGTGTTC AACAGATAGG CAATGCTTCC CACTAAGACT TGAATCTTGC	1553
CTTTACCCCT TGCATGCCTC CCACCTGCTT CCCTGGATCC CAGGACAGCA GCATCCACCC	1613
CTTTCCAAAG GATTGAGAAA ATGGTAGCTA AGGTTACACC CATAGGACCT ACCACGTACC	1673
AAGCACTTCC ACACATATTA TCCCTTTTCA CCCTTAAAT AATCCTATAA GGTAGAAAAA	1733
AAAAAAAAA AAAAAAAAAA	1753

(2) INFORMATION FOR SEQ ID NO: 9:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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Met Asn Cys Ile Ser Asp Phe Phe Thr Tyr Glu Thr Thr Lys Ser Val
 1           5           10           15
Val Val Lys Ser Trp Thr Ile Gly Ile Ile Asn Arg Ala Val Gln Leu
          20           25           30
Leu Ile Ile Ser Tyr Phe Val Gly Trp Val Phe Leu His Glu Lys Ala
          35           40           45
Tyr Gln Val Arg Asp Thr Ala Ile Glu Ser Ser Val Val Thr Lys Val
          50           55           60
Lys Gly Phe Gly Arg Tyr Ala Asn Arg Val Met Asp Val Ser Asp Tyr
          65           70           75           80
Val Thr Pro Pro Gln Gly Thr Ser Val Phe Val Ile Ile Thr Lys Met
          85           90           95
Ile Val Thr Glu Asn Gln Met Gln Gly Phe Cys Pro Glu Asn Glu Glu
          100          105          110
Lys Tyr Arg Cys Val Ser Asp Ser Gln Cys Gly Pro Glu Arg Phe Pro
          115          120          125
Gly Gly Gly Ile Leu Thr Gly Arg Cys Val Asn Tyr Ser Ser Val Leu
          130          135          140
Arg Thr Cys Glu Ile Gln Gly Trp Cys Pro Thr Glu Val Asp Thr Val
          145          150          155          160
Glu Met Pro Ile Met Met Glu Ala Glu Asn Phe Thr Ile Phe Ile Lys
          165          170          175
Asn Ser Ile Arg Phe Pro Leu Phe Asn Phe Glu Lys Gly Asn Leu Leu
          180          185          190
Pro Asn Leu Thr Asp Lys Asp Ile Lys Arg Cys Arg Phe His Pro Glu
          195          200          205
Lys Ala Pro Phe Cys Pro Ile Leu Arg Val Gly Asp Val Val Lys Phe
          210          215          220
Ala Gly Gln Asp Phe Ala Lys Leu Ala Arg Thr Gly Gly Val Leu Gly
          225          230          235          240
Ile Lys Ile Gly Trp Val Cys Asp Leu Asp Lys Ala Trp Asp Gln Cys
          245          250          255
Ile Pro Lys Tyr Ser Phe Thr Arg Leu Asp Gly Val Ser Glu Lys Ser
          260          265          270

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58

Ser	Val	Ser	Pro	Gly	Tyr	Asn	Phe	Arg	Phe	Ala	Lys	Tyr	Lys	Met
		275					280					285		
Glu	Asn	Gly	Ser	Glu	Tyr	Arg	Thr	Leu	Leu	Lys	Ala	Phe	Gly	Arg
	290					295					300			
Phe	Asp	Val	Leu	Val	Tyr	Gly	Asn	Ala	Gly	Lys	Phe	Asn	Ile	Pro
305					310					315				320
Thr	Ile	Ile	Ser	Ser	Val	Ala	Ala	Phe	Thr	Ser	Val	Gly	Val	Thr
				325					330					335
Val	Leu	Cys	Asp	Ile	Ile	Leu	Leu	Asn	Phe	Leu	Lys	Gly	Ala	His
			340					345					350	
Tyr	Lys	Ala	Arg	Lys	Phe	Glu	Glu	Val	Thr	Glu	Thr	Thr	Leu	Gly
		355					360					365		
Thr	Ala	Ser	Thr	Asn	Pro	Val	Phe	Ala	Ser	Asp	Gln	Ala	Thr	Glu
	370					375					380			
Lys	Gln	Ser	Thr	Asp	Ser	Gly	Ala	Tyr	Ser	Ile	Gly	His		
385					390					395				

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: human P2x

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 174..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GCCTCCAGCT GACCTCTGGC TCCTGTCTC TGGCTCCACC TGCACCGCCC TGCTCTTCCT	60
AAGGGGCCAG GAAGCCCCA GAAGCTCTAC CATCGAAGTG GGTGGTGGCA CCCGGCTCAC	120
CCTGAGAGCA GAGGGCGTGC AGGGGGCTCA GTTCTGAGCC CAGCCGGCCC ACC ATG	176
	Met
GCA CGG CGG TTC CAG GAG GAG CTG GCC GCC TTC CTC TTC GAG TAT GAC	224
Ala Arg Arg Phe Gln Glu Glu Leu Ala Ala Phe Leu Phe Glu Tyr Asp	
400 405 410	
ACC CCC CGC ATG GTG CTG GTG CGT AAT AAG AAG GTG GGC GTT ATC TTC	272
Thr Pro Arg Met Val Leu Val Arg Asn Lys Lys Val Gly Val Ile Phe	
415 420 425 430	
CGA CTG ATC CAG CTG GTG GTC CTG GTC TAC GTC ATC GGG TGG GTG TTT	320
Arg Leu Ile Gln Leu Val Val Leu Val Tyr Val Ile Gly Trp Val Phe	
435 440 445	
CTC TAT GAG AAG GGC TAC CAG ACC TCG AGC GGC CTC ATC AGC AGT GTC	368
Leu Tyr Glu Lys Gly Tyr Gln Thr Ser Ser Gly Leu Ile Ser Ser Val	
450 455 460	
TCT GTG AAA CTC AAG GGC CTG GCC GTG ACC CAG CTC CCT GGC CTC GGC	416
Ser Val Lys Leu Lys Gly Leu Ala Val Thr Gln Leu Pro Gly Leu Gly	
465 470 475	
CCC CAG GTC TGG GAT GTG GCT GAC TAC GTC TTC CCA GCC CAG GGG GAC	464
Pro Gln Val Trp Asp Val Ala Asp Tyr Val Phe Pro Ala Gln Gly Asp	
480 485 490	
AAC TCC TTC GTG GTC ATG ACC AAT TTC ATC GTG ACC CCG AAG CAG ACT	512
Asn Ser Phe Val Val Met Thr Asn Phe Ile Val Thr Pro Lys Gln Thr	
495 500 505 510	

CAA GGC TAC TGC GCA GAG CAC CCA GAA GGG GGC ATA TGC AAG GAA GAC Gln Gly Tyr Cys Ala Glu His Pro Glu Gly Ile Cys Lys Glu Asp 515 520 525	560
AGT GGC TGT ACC CCT GGG AAG GCC AAG AGG AAG GCC CAA GGC ATC CGC Ser Gly Cys Thr Pro Gly Lys Ala Lys Arg Lys Ala Gln Gly Ile Arg 530 535 540	608
ACG GGC AAG TGT GTG GCC TTC AAC GAC ACT GTG AAG ACG TGT GAG ATC Thr Gly Lys Cys Val Ala Phe Asn Asp Thr Val Lys Thr Cys Glu Ile 545 550 555	656
TTT GGC TGG TGC CCC GTG GAG GTG GAT GAC GAC ATC CCG CGC CCT GCC Phe Gly Trp Cys Pro Val Glu Val Asp Asp Asp Ile Pro Arg Pro Ala 560 565 570	704
CTT CTC CGA GAG GCC GAG AAC TTC ACT CTT TTC ATC AAG AAC AGC ATC Leu Leu Arg Glu Ala Glu Asn Phe Thr Leu Phe Ile Lys Asn Ser Ile 575 580 585 590	752
AGC TTT CCA CGC TTC AAG GTC AAC AGG CGC AAC CTG GTG GAG GAG GTG Ser Phe Pro Arg Phe Lys Val Asn Arg Arg Asn Leu Val Glu Glu Val 595 600 605	800
AAT GCT GCC CAC ATG AAG ACC TGC CTC TTT CAC AAG ACC CTG CAC CCC Asn Ala Ala His Met Lys Thr Cys Leu Phe His Lys Thr Leu His Pro 610 615 620	848
CTG TGC CCA GTC TTC CAG CTT GGC TAC GTG GTG CAA GAG TCA GGC CAG Leu Cys Pro Val Phe Gln Leu Gly Tyr Val Val Gln Glu Ser Gly Gln 625 630 635	896
AAC TTC AGC ACC CTG GCT GAG AAG GGT GGA GTG GTT GGC ATC ACC ATC Asn Phe Ser Thr Leu Ala Glu Lys Gly Gly Val Val Gly Ile Thr Ile 640 645 650	944
GAC TGG CAC TGT GAC CTG GAC TGG CAC GTA CGG CAC TGC AGA CCC ATC Asp Trp His Cys Asp Leu Asp Trp His Val Arg His Cys Arg Pro Ile 655 660 665 670	992
TAT GAG TTC CAT GGG CTG TAC GAA GAG AAA AAT CTC TCC CCA GGC TTC Tyr Glu Phe His Gly Leu Tyr Glu Glu Lys Asn Leu Ser Pro Gly Phe 675 680 685	1040
AAC TTC AGG TTT GCC AGG CAC TTT GTG GAG AAC GGG ACC AAC TAC CGT Asn Phe Arg Phe Ala Arg His Phe Val Glu Asn Gly Thr Asn Tyr Arg 690 695 700	1088
CAC CTC TTC AAG GTG TTT GGG ATT CGC TTT GAC ATC CTG GTG GAC GGC His Leu Phe Lys Val Phe Gly Ile Arg Phe Asp Ile Leu Val Asp Gly 705 710 715	1136
AAG GCC GGG AAG TTT GAC ATC ATC CCT ACA ATG ACC ACC ATC GGC TCT Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met Thr Thr Ile Gly Ser 720 725 730	1184
GGA ATT GGC ATC TTT GGG GTG GCC ACA GTT CTC TGT GAC CTG CTG CTG Gly Ile Gly Ile Phe Gly Val Ala Thr Val Leu Cys Asp Leu Leu Leu 735 740 745 750	1232

CTT CAC ATC CTG CCT AAG AGG CAC TAC TAC AAG CAG AAG AAG TTC AAA Leu His Ile Leu Pro Lys Arg His Tyr Tyr Lys Gln Lys Lys Phe Lys	1280
755 760 765	
TAC GCT GAG GAC ATG GGG CCA GGG GCG GCT GAG CGT GAC CTC GCA GCT Tyr Ala Glu Asp Met Gly Pro Gly Ala Ala Glu Arg Asp Leu Ala Ala	1328
770 775 780	
ACC AGC TCC ACC CTG GGC CTG CAG GAG AAC ATG AGG ACA TCC Thr Ser Ser Thr Leu Gly Leu Gln Glu Asn Met Arg Thr Ser	1370
785 790 795	
TGATGCTCGG GCCCCAACTC CTGACTGGGT GCAGCGTGAG GCTTCAGCCT GGAGCCCTGG	1430
TGGGTCCCAG CCAGGGCAGA GGGGCTCCC CAGGAAGTCT CCTACCTCT CAGCCAGGCA	1490
GAGAGCAGTT TGCCAGAAGC TCAGGGTGCA TAGTAGGAGA GACCTGTGCA AATCTGAGCT	1550
CCGGCTCCGA CCCCACACAC CCTGAGGGAG GCCTACCTA GCCTCAGCCG CTCCTGGTGG	1610
GGGAATGGCT GGGGGTTGGG CAGGACCTC CCACACACCT GCACCTAGC TTCGTGCTTC	1670
TCTCTCCGGA CTCTCATTAT CCAACCCGCT GCCTCCATTT CTCTAGATCT GTGCTCTCCG	1730
ATGTGGCAGT CAGTAACCAT AGGTGACTAA ATTAACTAA AATAAAATAG AATGAAACAC	1790
AAAATTCAAT TCCTCGGCTG AACTAGCCAC ATTTCAACTG CTCAGTAGAT ACGTGTGGTT	1850
AGTGGCTGCC ATACTGGACA GCTCGGGGCA TTTTCACTGT CAAAGAAAAT TCTATTAGAC	1910
AGCCCTGCTT GAGCCCTGTT TCTTCTGGC TTCGGTTTCC CTGGGGAAT TATCGACAAT	1970
GCAAGCTCCT GGGCCCAACC CCAGACCTCC TGAACCAAAA GCTCCAGGGC TGGCCGTATG	2030
ATCTGTGTGG ATGGCAAACCT CCCCAGGCCA TTCTGGGACC TAAGTTTAAG AAGTGCCGTC	2090
CTCGAACTTT CTGACTCTAA GCTCCTGAGC GGGAGTCAGA CTTAGCCCTG AGCCTGCACT	2150
TCCTGTTTCTG GTGCAGACAC TGAACAGGGT CTCAAACACC TTCAGCATGT GTGTTGTGTG	2210
CTCAGTGCC ACACAGTGTC TCATGCACAC AACCCAGTGT ACACACCACC TACGTGCACA	2270
CAGCATCCTT CCACACTGTG TATGTGAACA GCTTGGGCCC TGCAAACACA ACCATCTACA	2330
CACATCTACA CCCCCAAGCA CACACACATG GTCCGTGCCA TGTCACCTCC ATAGGGAAG	2390
GCTTCTCTCC AAGTGTGCCA GGCCAGGACA GCCCTCCAG CCATGAATCC TTA CTGAGCT	2450
ACCTCGGGTT GGGGTGGGAG CCCCAGCCAA ATCCTGGGCT CCCTGCCTGT GGCTCAGCCC	2510
CAGCTCCCAA GGCCTGCCTG GCTCTGTCTG AACAGAAGGT CTGGGGGAAG CGAGGGGTGG	2570
AGTACAATAA AGGGAATGAG GACAAACAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2630
AAAAAAAAAA AAA	2643

(2) INFORMATION FOR SEQ ID NO: 11:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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Met Ala Arg Arg Phe Gln Glu Glu Leu Ala Ala Phe Leu Phe Glu Tyr
 1      5      10      15
Asp Thr Pro Arg Met Val Leu Val Arg Asn Lys Lys Val Gly Val Ile
      20      25      30
Phe Arg Leu Ile Gln Leu Val Val Leu Val Tyr Val Ile Gly Trp Val
      35      40      45
Phe Leu Tyr Glu Lys Gly Tyr Gln Thr Ser Ser Gly Leu Ile Ser Ser
      50      55      60
Val Ser Val Lys Leu Lys Gly Leu Ala Val Thr Gln Leu Pro Gly Leu
      65      70      75      80
Gly Pro Gln Val Trp Asp Val Ala Asp Tyr Val Phe Pro Ala Gln Gly
      85      90      95
Asp Asn Ser Phe Val Val Met Thr Asn Phe Ile Val Thr Pro Lys Gln
      100      105      110
Thr Gln Gly Tyr Cys Ala Glu His Pro Glu Gly Gly Ile Cys Lys Glu
      115      120      125
Asp Ser Gly Cys Thr Pro Gly Lys Ala Lys Arg Lys Ala Gln Gly Ile
      130      135      140
Arg Thr Gly Lys Cys Val Ala Phe Asn Asp Thr Val Lys Thr Cys Glu
      145      150      155      160
Ile Phe Gly Trp Cys Pro Val Glu Val Asp Asp Asp Ile Pro Arg Pro
      165      170      175
Ala Leu Leu Arg Glu Ala Glu Asn Phe Thr Leu Phe Ile Lys Asn Ser
      180      185      190
Ile Ser Phe Pro Arg Phe Lys Val Asn Arg Arg Asn Leu Val Glu Glu
      195      200      205
Val Asn Ala Ala His Met Lys Thr Cys Leu Phe His Lys Thr Leu His
      210      215      220
Pro Leu Cys Pro Val Phe Gln Leu Gly Tyr Val Val Gln Glu Ser Gly
      225      230      235      240
Gln Asn Phe Ser Thr Leu Ala Glu Lys Gly Gly Val Val Gly Ile Thr
      245      250      255
Ile Asp Trp His Cys Asp Leu Asp Trp His Val Arg His Cys Arg Pro
      260      265      270

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Ile Tyr Glu Phe His Gly Leu Tyr Glu Glu Lys Asn Leu Ser Pro Gly
 275 280 285
 Phe Asn Phe Arg Phe Ala Arg His Phe Val Glu Asn Gly Thr Asn Tyr
 290 295 300
 Arg His Leu Phe Lys Val Phe Gly Ile Arg Phe Asp Ile Leu Val Asp
 305 310 315 320
 Gly Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met Thr Thr Ile Gly
 325 330 335
 Ser Gly Ile Gly Ile Phe Gly Val Ala Thr Val Leu Cys Asp Leu Leu
 340 345 350
 Leu Leu His Ile Leu Pro Lys Arg His Tyr Tyr Lys Gln Lys Lys Phe
 355 360 365
 Lys Tyr Ala Glu Asp Met Gly Pro Gly Ala Ala Glu Arg Asp Leu Ala
 370 375 380
 Ala Thr Ser Ser Thr Leu Gly Leu Gln Glu Asn Met Arg Thr Ser
 385 390 395

CLAIMS

1. A recombinant or isolated DNA molecule encoding a P_{2X} receptor, wherein the receptor:
- 5 (a) has the amino sequence shown in Figure 1, Figure 2, Figure 3 or Figure 4; or
- (b) is substantially homologous to the sequence shown in Figure 1, Figure 2, Figure 3 or Figure 4;
- 10 or a fragment of such a DNA molecule, which fragment includes at least 15 nucleotides taken from nucleotides 1 to 813 shown in Figure 1, from the full nucleotide sequences shown in Figures 2 and 3, or from nucleotides 1 to 1744 shown in Figure 4.
2. A recombinant or isolated DNA molecule encoding a P_{2X} receptor, wherein the receptor:
- 15 (a) has the amino sequence shown in Figure 1 or Figure 4; or
- (b) is substantially homologous to the sequence shown in Figure 1 or Figure 4;
- 20 or a fragment of such a DNA molecule, which fragment includes at least 15 nucleotides taken from nucleotides 1 to 813 shown in Figure 1 or from nucleotides 1 to 777 shown in Figure 4.
3. A recombinant or isolated DNA molecule encoding a P_{2X} receptor, wherein the receptor:
- 25 (a) has the amino sequence shown in Figure 1; or
- (b) is substantially homologous to the sequence shown in Figure 1;
- or a fragment of such a DNA molecule, which fragment includes at least 15 nucleotides taken from nucleotides 1 to 813 shown in Figure 1.

4. A DNA molecule as claimed in any of claims 1 to 3,
which encodes a human P_{2X} receptor.
5. A DNA molecule as claimed in any of claims 1 to 4,
5 which is cDNA.
6. A DNA molecule as claimed in any of claims 1 to 5,
which is in the form of a vector.
- 10 7. A host cell transformed or transfected with a vector
as described in claim 6.
8. A host cell as claimed in claim 7 which is a stably
transfected mammalian cell which expresses a P_{2X} receptor.
15
9. A preparation of P_{2X} receptor which is free of
protein with which it is naturally associated.
10. A preparation of P_{2X} receptor which is free of P_{2Y}
20 receptor.
11. P_{2X} receptor as prepared by recombinant DNA
technology.
- 25 12. A peptide fragment of P_{2X} receptor which includes an
epitope which is immunologically non-cross reactive with
the RP-2 polypeptide disclosed in Owens et al. (*loc.*
cit.).
- 30 13. An antibody which is specific for an epitope of P_{2X}
receptor which is immunologically non-cross reactive with
the RP-2 polypeptide disclosed in Owens et al. (*loc.*
cit.).

14. An antibody as claimed in claim 13, which is a monoclonal antibody.

5 15. A cell expressing an antibody as claimed in claim 14.

10 16. The use of a P_{2X} receptor or a preparation thereof, as claimed in claim 7, 8 or 9, as a screen for compounds useful in the treatment or prophylaxis of a human or non-human animal disease or condition.

15 17. The use of a P_{2X} receptor or a preparation thereof as claimed in claim 9, 10 or 11 as a screen for identifying a P_{2X} agonist or a P_{2X} antagonist.

18. A P_{2X} agonist or a P_{2X} antagonist identified by a screen as described in claim 17.

20 19. A method for obtaining a DNA molecule according to claim 1, wherein the molecule is obtained by chemical synthesis or by using recombinant DNA technology.

25 20. A method for obtaining a P_{2X} receptor comprising expressing the P_{2X} receptor using a host cell according to claim 8 and, optionally, purifying the P_{2X} receptor.

30 21. A DNA molecule, a P_{2X} receptor, a P_{2X} agonist or a P_{2X} antagonist, a method, or a use, substantially as hereinbefore described, with reference to the accompanying examples.

1/15

FIGURE 1**P2x0.1 cDNA from rat vas deferens**

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1  gccaaaagctgtctgatcaccagggttttctccaaaccagaccaccatcgaaacctccaaactcgggtccacct 80
81  agcctgtctgtccttaaggggccgggaagccagtcactccactgtattgagatgcagatggtggcctgcccttga 160
161  ccatagagggcgtgtgggtgttcattctctgtgcccccttctggcccccc  ATG GCT CGG CGG CTG CAA GAT  230
      1      M  A  R  R  L  Q  D  7
231  GAG CTG TCA GCC TTC TTC TTT GAA TAT GAC ACT CCC CGG ATG GTG CTG GTA CGA AAC AAG  290
      8  E  L  S  A  F  F  E  Y  D  T  P  R  M  V  L  V  R  N  K  27
291  AAG GTG GGA GTC ATT TTC CGT CTG ATC CAG TTG GTG GTT CTG GTC TAC GTC ATT GGG TGG  350
      28  K  V  G  V  I  F  R  L  I  O  L  V  V  L  V  Y  V  I  Q  W  47
351  GTG TTT GTG TAT GAA AAA GGA TAC CAG ACC TCA AGT GAC CTC ATC AGC AGT GTG TCC GTG  410
      48  V  F  V  Y  E  K  G  Y  Q  T  S  S  D  L  I  S  S  V  57
411  AAG CTC AAG GGC TTG GCT GTG ACC CAG CTC CAG GGC CTG GGA CCC CAG GTC TGG GAC GTG  470
      68  K  L  K  G  L  A  V  T  Q  L  Q  G  L  G  P  Q  V  W  D  V  87
471  GCT GAC TAT GTC TTC CCA GCA CAC GGG GAC AGC TCC TTT GTA GTT ATG ACC AAC TTC ATC  530
      88  A  D  Y  V  F  P  A  H  G  D  S  S  F  V  V  M  T  N  F  I  107
531  GTG ACC CCT CAG CAG ACT CAA GGC CAT TGT GCA GAG AAC CCA GAA GGT GGC ATA TGC CAG  590
      108  V  T  P  Q  Q  T  Q  G  H  C  A  E  N  P  E  G  I  C  Q  127
591  GAT GAC ACT GGC TGC ACT CCA GGA AAA GCA GAA AGG AAA GCC CAA GGT ATT CGC ACA GGC  650
      128  D  D  S  G  C  T  P  G  K  A  E  R  K  A  Q  G  I  R  T  G  147
651  AAC TGT GTG CCC TTC AAT GGC ACT GTG AAG ACA TGT GAG ATC TTT GGT TGG TGT CCT GTA  710
      148  N  C  V  P  F  N  G  T  V  K  T  C  E  I  F  G  W  C  P  V  167
711  GAG GTG GAT GAC AAG ATC CCA AGC CCT GCT CTT CGT GAG GCT GAG AAC TTC ACC CTC  770
      168  E  V  D  D  K  I  P  S  P  A  L  L  R  E  A  E  N  F  T  L  187
      CCC CAG CTG GCA CAT GGC TGC TAC CCA TGC CCT CCA CAC AG
      P  Q  L  A  H  G  C  Y  P  C  P  H  R  sequence of RP-2

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FIGURE 1 (cont'd)

[illegible]

rat P2X clone 3

FIGURE 2

1	cgcagcgagcctgccggagctggtgggtggagctatcgacccggaggccgacggtggcgaggggccccacagtgtcccagggc	80	
81	gcggagcggtcggcgagacc	ATG GCG GGC TGC TGC C C S V L G S F L P E Y	145
16	D T P R I V L I R S R K V G L M N R A V	205	
146	GAC ACG CGC ATC GTG CTC ATC CGC AGC CGT AAA GTG GGG CTC ATG AAC CGC GCG GTG	35	
206	CAG CTG CTC ATC CTG GCT TAC GTG ATC GGG TGG GTG TTC GTG TGG GAA AAG GGC TAC CAG	265	
36	Q L I L A Y V I G W V F V W E K G Y Q	55	
266	GAA ACG GAC TCC GTG GTC AGC TCG CTG ACA ACC AAA GCC AAA GGT GTG GCT GTG ACC AAC	325	
56	E T D S V V S S V T T K A K G V A V T N	75	
326	ACC TCT CAG CTT GGA TTC CGG ATC TGG GAC GTG GCG GAC TAT GTG ATT CCA GCT CAG GAG	385	
76	T S Q L G F R I W D V A D Y V I P A Q E	95	
386	GAA AAC TCC CTC TTC ATT ATG ACC AAC ATG ATT GTC ACC GTG AAC CAG ACA CAG AGC ACC	445	
96	E N S L F I M T N H I V T V N Q T Q S T	115	
446	TGT CCA GAG ATT CCT GAT AAG ACC AGC ATT TGT AAT TCA GAC GCC GAC TGC ACT CCT GGC	505	
116	C P E I P D K T S I C N S D A D C T P G	135	
506	TCC GTG GAC ACC CAC AGC AGT GGA GTT GCG ACT GGA AGA TGT GTT CCT TTC AAT GAG TCT	565	
136	S V D T H S S G V A T G R C V P F N E S	155	
566	GTG AAG ACC TGT GAG GTG GCT GCA TGG TGC CCG GTG GAG AAC GAC GTT GGC GTG CCA ACG	625	
156	V K T C E V A A W C P V E N D V G V P T	175	
626	CGG GCT TTC ATA AAG GCT GCA GAA AAC TTC ACC CTC TTG GTA AAG AAC AAC ATC TGG TAC	685	
176	P A F L K A A E N F T L L V K N N I W Y	195	
686	CCC AAG TTT AAC TTC AGC AAG AGG AAC ATC CTC CCC AAC ATC ACC AGC TCC TAC CTC AAA	745	
196	P K F H F S K R N I L P N I T T S Y L K	215	
746	TGG TGC ATT TAC AAT GCT CAA ACG GAT CCC TTC TGC CCC AWA TTC CGT CTT GGC ACA ATC	805	
216	S C I Y N A Q T D P F C P I F R L G T I	235	

FIGURE 2 (cont'd)

806 GTG GGG GAC GCG GGA CAT AGC TTC CAG GAG ATG GCA GTT GAG GGA GGC ATC ATG GGT ATC 865
 236 V G D A G H S F Q E M A V E G G I M G I 255
 866 CAG ATC AAG TGG GAC TGC AAC CTG AAC GAT AGA GGC GGC TCC CTT TGC CTG CCC AGA TAT TCC 925
 256 Q I K W D C N L D R A A S L C L P R Y S 275
 926 TTC CGG CGC CTG GAC ACC CGG GAC CTG GAA CAC AAT GTG TCT CCT GGC TAC AAT TTC AGG 985
 276 F R R L D T R D L E H N V S P G Y N F R 295
 986 TTT GGC AAG TAC TAC AGG GAC CTG GCC GGC AAA GAG CAG CGC ACA CTC ACC AAG GCG TAC 1045
 296 F A K Y Y R D L A G K E Q R T L T K A Y 315
 1046 GGC ATC CGC TTT GAC ATC ATC GTG TTT GGA AAG GCT GGG AAG TTT GAC ATC ATC CCT ACC 1105
 316 G I R F D I I V F G K A G K F D I I P T 335
 1106 ATG ATC AAC GTT GGC TCT GGC TTG GCG CTC CTC GCG GTG GCG ACG GTG CTC TGT GAC GTC 1165
 336 M I N V G S G L A L G V A T V L C D V 355
 1166 ATA GTC CTC TAC TGC ATG AAG AAG AAA TAC TAC CCG GAC AAG AAA TAT AAG TAT GTG 1225
 356 I V L Y C M K K Y Y R D K K Y K Y V 375
 1226 GAA GAC TAC GAG CAG GGT CTT TCG GCG GAG ATG AAC CAG TGA CGCTAAGTTACATTCCACCCC 1291
 376 E D Y E Q G L S G E M N Q 389
 1292 gctcagcccggaagcagaagatgggagagatggctactgctctgctcactctagagaaagctccagagtttcagctc 1371
 1372 agttctccactccacaatactcaggggttgccaaagcacatcttgctggagcccggtcttgctctgctgctcagatgggc 1451
 1452 ttccagatacaagaatcctctctgctctctaggaatgctgggatacaacatgtcacttgcaatgcccatcttcccat 1531
 1532 gggagcttgggcatcttttacatctttaccctttctctctgtatcatctaaaggctgccctcagcagacagcttcttcc 1611
 1612 accctatacaccctcttaatctcactgtgtggtggaggggggtgcttgcacacgacgacgacgctgctgctgctgct 1691
 1692 gttggctgggcccacctgtggttatacagtgtagcgtatggaggttaggaagggctctgagagagacactgctgtggc 1771
 1772 ttacggacagggccaggctctgtccacgaccttattcttaaggaaggaggtctctcaggtgctgctcagcagggcctggg 1851
 1852 acaccattctctctccctataatcagagaggtgtccctgttagcaaggcaggggttagcttctctctctataagggtctg 1931
 1932 gttgaatgacctaggaccacaacattaaagaataattttttaaaaaaataaaaaa 1997

5 / 15

FIGURE 3

rat P2X clone 6

1 cactgggtacagttgctgggtacaggaactgggtctcttctcaagcctcattaaagcagccactccagttcttgat 80
 81 ctttgctctccagtcctgaagtctcttca 160
 161 gt atg aac tgt ata tca gac ttc ttc acc tac gag act acc aag tgc gtt gtt gng aag 219
 1 m n c i s d f f t y e t t k s v v v k 19
 220 agc tgc acc att ggg atc atc aac cga gcc gtc cag ctg att atc ttc tac ttt gng 279
 20 s w t i g i i n r a v q l l i i s y f v 39
 280 ggg tgg gtt ttc ttc cat gag aag gcc tac caa gtg agg gac acc gcc att gag tcc tca 339
 40 g w v f l h e k a y q v r d t a i e s s 59
 340 gta gtt aca aag gtg aaa ggc ttc ggg cgc tat gcc aac aga gtc atg gac gtg tgc gat 399
 60 v v t k v k g f g r y a n r v m d v s d 79
 400 tat gtg acc cca gcc cag gcc acc tct gtc ttt gtc atc atc acc aaa atg atc gtt act 459
 80 y v t p p q g t s v f v i i t k m i v t 99
 460 gaa aat caa atg caa gga ttc tgt cca gag aat gaa gag aag tac gcc tgt gtg tct gac 519
 100 e n q m q g f c p e n e k y r c v s d 119
 520 agc cag tgt ggg cct gaa cgc ttc cca ggt ggg atc ctg acc ggc cgc tgc gtg aac 579
 120 s q c g p e r f p g g i l t g r c v n 139
 580 tac agc tct gtt ctg cgg acc tgt gag atc cag ggc tgg tgc gcc act gag gtg gac acc 639
 140 y s s v l r t c e i q g w c p t e v d t 159
 640 gtg gag atg cct atc atg atg gag gct gag aac ttc acc att ttc atc aag aac agc atc 699
 160 v e m p i m m e a e n f t i f i k n s i 179
 700 ggt ttc cct ctg ttc aac ttt gag aag gga aac ctg cct aac ctg acc gac aag gac 759
 180 r f p l f n f e k g n l l p n l t d k d 199
 760 ata aag agg tgc cgc ttc cac cct gaa abg gcc cca ttt tgc gcc atc ttc agg gta ggg 819
 200 i k r c r f f h p e k a p f c p i l r v g 219

6 / 15

FIGURE 3 (cont'd)

820 GAT GTC GTT AAG TTT GCT GGA CAG GAT TTT GCT AAG CTG GCC AGC GGT GGC GTT CTG 879
 220 D V V K F A G Q D F A K L A R T G G V L 239
 880 GGT ATT AAG ATC GGC TGG GTG TGC GAT CTA GAC AAG GCC TGG GAC FAG TGC ATC CCT AAA 939
 240 G I K I G W V C D L D K A W D Q C I P K 259
 940 TAT TCC TTC ACT CGG CTG GAT GGA GTT TCT TCT GAG AAA AGC AGT GTT TCC CCT GGC TAC AAC 999
 260 Y S F T R L D G V S E K S S V S P G Y N 279
 1000 TTC AGG TTT GCC AAA TAC TAT AAG ATG GAG AAC GGC AGC GAG TAC CGC ACA CTC CTG AAG 1059
 280 F R F A K Y Y K M E N G S E Y R T L L K 299
 1060 GCT TTT GGC ATC GGC TTT GAT GTG CTG GTA TAT GGG AAC GCT GGC AAG TTC AAC ATC ATC 1119
 300 A F G I R F D V L V Y G N A G K F N I I 319
 1120 CCC ACC ATT ATC AGC TCG GTG GCG GGC TTC ACT TCT GTG GGA GTG GGC ACT GTT CTC TGT 1179
 320 P T I I S S V A A F T S V G V G T V L C 339
 1180 GAC ATC ATC CTG CTC AAT TTC CTC AAA GGG GCT GAT CAC TAC AAA GCC AGG AAG TTT GAG 1239
 340 D I I L L N F L K G A D H Y K A R K F E 359
 1240 GAG GTG ACT GAG ACA ACA CTG AAG GGT ACT GCG TCA ACC AAC CCA GTG TTC GCC AGT GAC 1299
 360 E V T E T T L K G T A S T N P V F A S D 379
 1300 CAG GCC ACT GTG GAG AAG CAG TCT ACA GAC TCA GCG GCC TAT TCT ATT GGT CAC tagggcct 1361
 380 Q A T V E K Q S T D S G A Y S I G H 397
 1362 cttccagggttcacatgctcaccccttaggtgcagaacctgcaaacaggccactctatctaaagcagtcaggggtggagg 1441
 1442 gggagaagaagggtctgtatttctgtgttccaccccaagactagatccagatatctaggccctcactgttcaacagata 1521
 1522 ggcaatgcttccactaagacttgaaatcttgcctttacccttgcattgcctccaccctgcttccctggatcccgagacag 1601
 1602 cagcatccaccccttccaaaggattgagaaaatggtagtaaggttacaccataggacctaccacgtaccaagcactt 1681
 1682 ccacacacattatcccttttccaccttaaaataatctctataaggttagaaaaaaataaaaaaa 1753

FIGURE 4

1 gcctccagctgaacctctgtgtctctgtctctgtgtccacctgaaccgacctgtctctcttaaggggccaggaaagccccc 80
 81 gaagctctaccatcgacgtggtggtgtggcaccctggtccacctgagagcagagggcgctgcagggggtcagttcttgagcc 160
 161 cagccggccacc ATG GCA CGG CCG TTC CAG GAG GAG CTG GCC GTC TTC CTC TTC GAG TAT 221
 1 H A R R F Q E E L A A F L F E Y 16
 222 GAC ACC CCC CGC ATG GTG CTG GTG CGT AAT AAG AAG GTG GGC GTT ATC TTC CGA CTG ATC 281
 17 D T P R M V L V R N K K V G V I F R L I 36
 282 CAG CTG GTG CTG GTG TAC GTC ATC GGG TGG GTG TTT CTC TAT GAG AAG GGC TAC CAG 341
 37 Q L V V L V Y V I G W V F L Y E K G Y Q 56
 342 ACC TCG AGC GGC CTC ATC AGC AGT GTC TCT GTG AAA CTC AAG GGC CTG GCC GTG ACC CAG 401
 57 T S S G L I S S V S V K L K G L A V T Q 76
 402 CTC CCT GGC CTC GGC CCC CAG GTC TGG GAT GTG GCT GAC TAC GTC TTC CCA GCC CAG GGG 461
 77 L P G L G P Q V W D V A D Y V F P A Q G 96
 462 GAC AAC TCC TTC GTG GTC ATG ACC AAT TTC ATC GTG ACC CCG AAG CAG ACT CAA GGC TAC 521
 97 D N S F V V M T N F I V T P K Q T Q G Y 116
 522 TGC GCA GAG CAC CCA GAA GGG GGC ATA TGC AAG GAA GAC AGT GGC TGT ACC CCT GGG AAG 581
 117 C A E H P E G G I C K E D S G C T P G K 136
 582 GCC AAG AGG AAG GCC CAA GGC ATC CGC ACG GGC AAG TGT GTG GCC TTC AAC GAC ACT GTG 641
 137 A K R K A Q G I R T G K C V A F N D T V 156
 642 AAG ACG TGT GAG ATC TTT GGC TGG TGC CCC GTG GAG GTG GAT GAC GAC ATC CCG CGC CCT 701
 157 K T C E I F G G W C P V E V D D I P R P 176

7/15

FIGURE 4 (cont'd)

702 GCC CTT CTC CGA GAG GCC GAG AAC TTC ACT CTT TTC ATC AAG AAC AGC ATC AGC TTT CCA 761
 177 A L L R E A E N F T L F I K N S I S F P 196

 762 CGC TTC AAG GTC AAC AGG CGC AAC CTG GTG GAG GAG AAT GCT GCC CAC ATG AAG ACC 821
 197 R F K V N R R N L V E E V N A A H M K T 216

 822 TGC CTC TTT CAC AAG ACC CTG CAC CCC CTG TGC CCA GTC TTC CAG CTT GGC TAC GTG GTG 881
 217 C L F H K T L H P L C P V F Q L G Y V V 236

 882 CAA GAG TCA GGC CAG AAC TTC AGC ACC CTG GCT GAG AAG GGT GGA GTG GTT GGC ATC ACC 941
 237 Q E S G Q N F S T L A E K G G V V G I T 256

 942 ATC GAC TGG CAC TGT GAC CTG GAC TGG CAC GTA CGG CAC TGC AGA CCC ATC TAT GAG TTC 1001
 257 I D W H C D L D W H V R H C R P I Y E F 276

 1002 CAT GGG CTG TAC CAA GAG AAA AAT CTC TCC CCA GGC TTC AAC TTC AGG TTT GCC AGG CAC 1061
 277 H G L Y E E K N L S P G F N F R F A R H 296

 1062 TTT GTG GAG AAC GGG ACC AAC TAC TAC CGT CAC CTC TTC AAG GTG TTT GGG ATT CGC TTT GAC 1121
 297 F V E N G T N Y R H L F K V F G I R F D 316

 1122 ATC CTG GTG GAC GGC AAG GCC GGG AAG TTT GAC ATC ATC CCT ACA ATG ACC ACC ATC GGC 1181
 317 I L V D G K A G K F D I I F T M T T I G 336

 1182 TCT GGA ATT GGC ATC TTT GGG GTG GCC ACA GTT CTC TGT GAC CTG CTG CTG CTT CAC ATC 1241
 337 S G I G I F G V A T V L C D L L L L H I 356

 1242 CTG CCT AAG AGG CAC TAC AAC CAG AAG AAC TTC AAA TAC GCT GAG GAC ATG GGG CCA 1301
 357 L P K R H Y Y K Q K K F K Y A E D M G P 376

 1302 GGG GCG GCT GAG CGT GAC CTC GCA GCT ACC AGC TCC ACC CTG GGC CTG CAG GAG AAC ATG 1361
 377 G A A E R D L A A T S S T L G L Q E N M 396

9 / 15

1362 AGG ACA TCC TGA TGCTGGGGCCCCCAACTCCTGACTGGGTGCAGCGGTGAGGCTTCAGCCCTGGAGCCCTGGGTGGGGTCC 1437
397 R T S . 400

1438 CAGTCAGGGCAGAGGGGGCTCCCCAGGAAGTCTCTACCCCTCTACGCCAGGCAGAGAGCAGTCTTGCCAGAGCTCAGGGT 1517
1518 GCATAGTAGGAGAGACCTGTGCAAACTCTGAGCTCCGGCTCCGAGCCCAACACACACCTCTGAGGGAGGGCTACCTCAGCCTCAG 1597
1598 CCGCTCCCTGGTCTGGGGGAAATGGCTGGGGGTCTGGGCAGGAGACCTCCCAACACCTGCAACCTAGCTCTGCTGCTCTCTCTCTCC 1677
1678 GGACTCTCATTATCCAACCCGCTGCTCTCAATCTCTCTAGATCTGTGCTCTCTCGATGTCGTCAGTCAATCAGTCACTAGGTGAC 1757
1758 TAAATTAACCTAAATATAAATAGAAATGAAACACAAAATCTCAATCTCTCGGCTGAACCTAGCCACATCTCAACCTGCTCAGTA 1837
1838 GATACGCTGTGGTCTAGTGGCTGGCATACTCGACAGCTCTGGGGCACTTCTCACTGTCAAGAAAGTCTCTATCAGACAGCCCTG 1917
1918 CTTGAGCCTGTCTCTCTCGGCTCTCGGTCTCTCGTGGGGAACCTTATCGACAAATGCAAGCTCCTCTGGGCCCAACCCCAAGACC 1997
1998 TCCGAAACCAAGCTCCAGGGCTGGCGTATGATCTGTGGGATGGCAACCTCCCAAGGCCATCTCTGGGAGCCTAAGTCTT 2077
2078 AAGAAGTGCCTCCCTCGAACTTCTGACTCTCAAGCTCTCTGAGCTCTCTGAGCTGAGGTCAGACTTAGCCCTGAGCTCTCCTGTT 2157
2158 CAGGTGCAGACACTGAACAGGGTCTCAACACCTCTCAGCATGTGTGTGTGTGCTCACGTGCTCCACACAGTGTCTCTCATGCA 2237
2238 CACAACCCAGTGTACACACCCACCTACGTGCACACAGCATCCTCTCAACACTGTGTATGTGAACAGCTCTGGGCCCTGTGCAAC 2317
2318 ACAACCATCTACACACATCTACACCCCAAGCACACACACATGGTCTCGTGCATGTCACTCTCCAATAGGGGAAGGCTCTCTC 2397
2398 TCCAAGTGTGCAAGGCCAGGACAGCCCTCCCAAGCCTGAATCCTTACTCAGTCACTCTGGGTCTGGGGTGGGAGCCCCAGC 2477
2478 CAAATCCTGGGTCTCTGTGTGGTCTCAGCCCCAGCTCCCCAAGGCTCTCTGCTCTGAACTGAGGAGGCTCTCTGGGG 2557
2558 AAGCGAGGGGTGGAGTACAATAAGGGGAAATGAGGACAAACAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2637
2638 AAAAA 2643

10 / 15

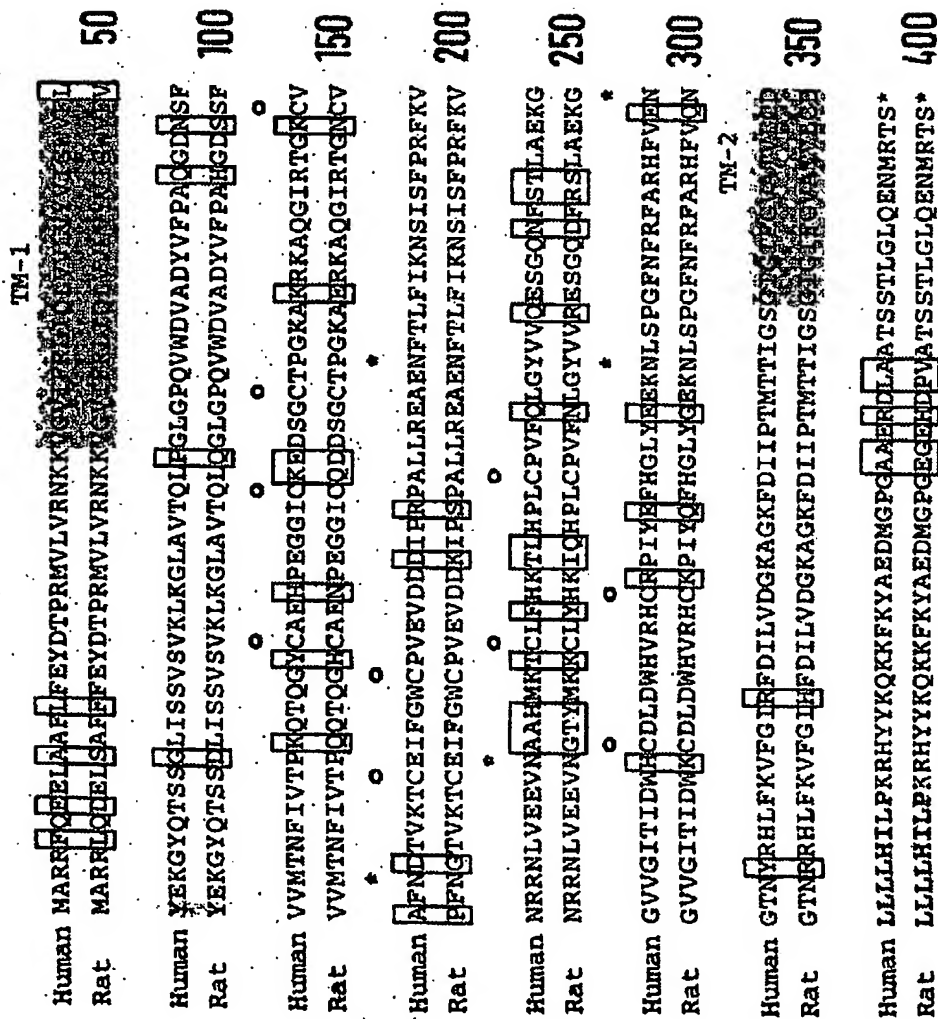


FIGURE 5

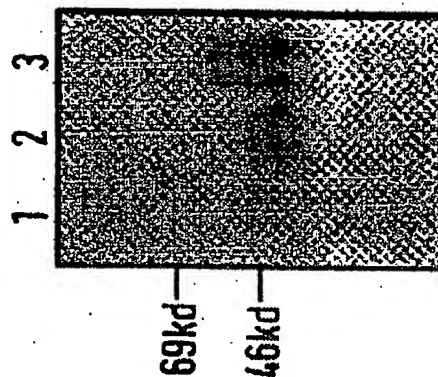


FIGURE 6

11 / 15

FIGURE 7

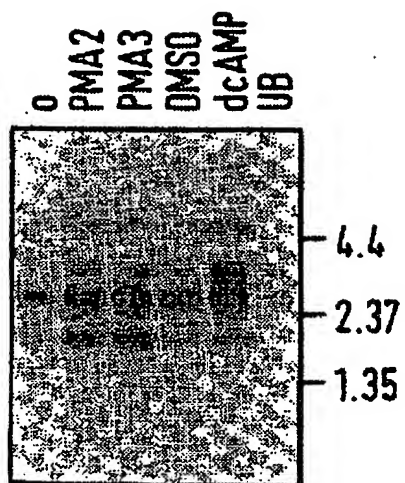
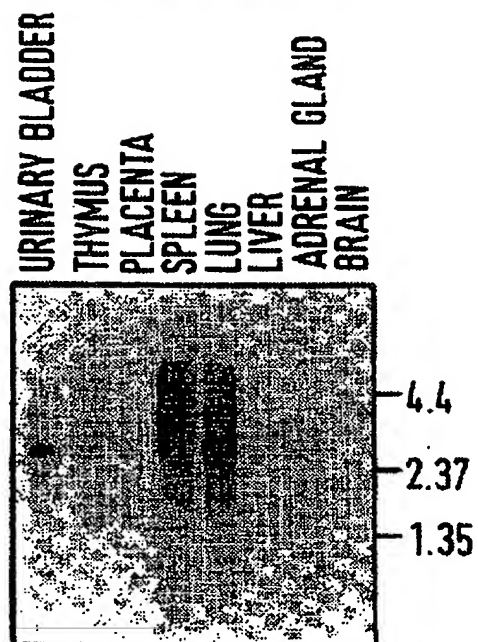


FIGURE 8



12 / 15

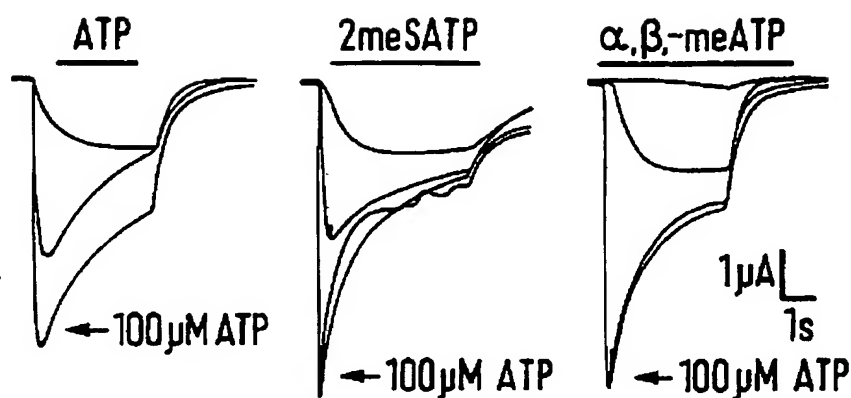


FIGURE 9

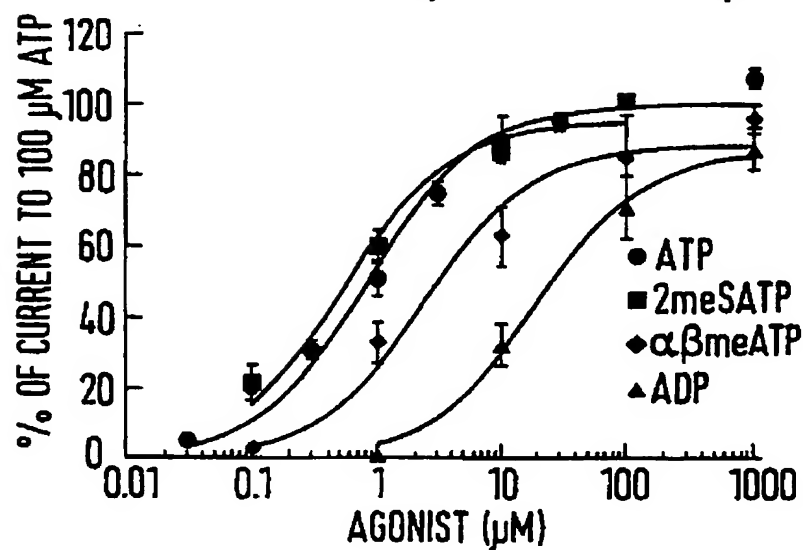


FIGURE 10

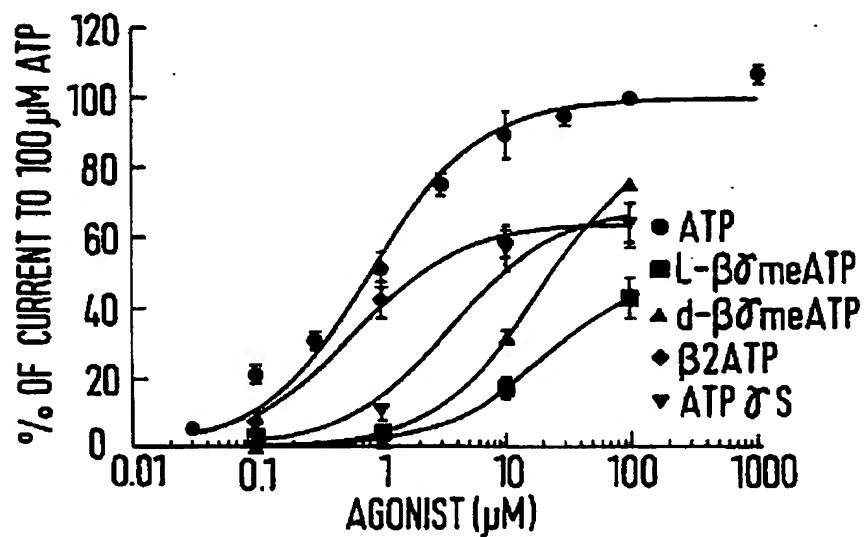


FIGURE 11

13 / 15

FIGURE 12

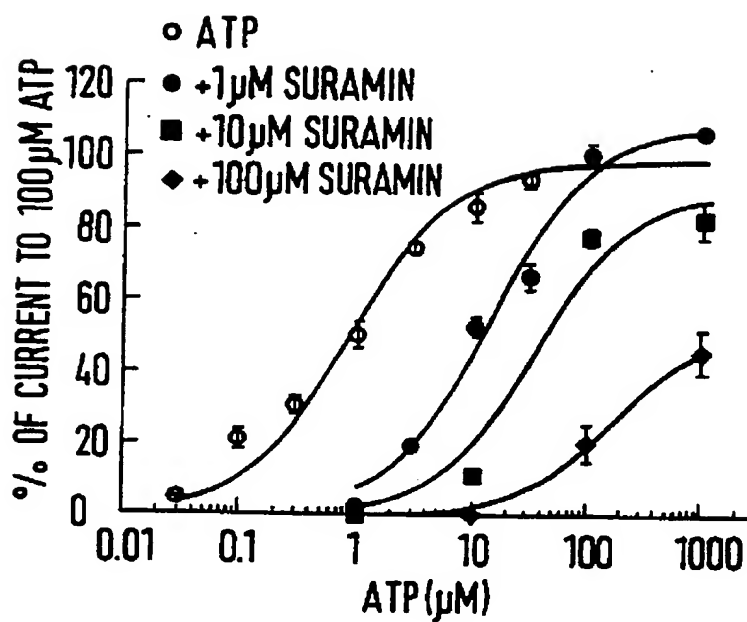
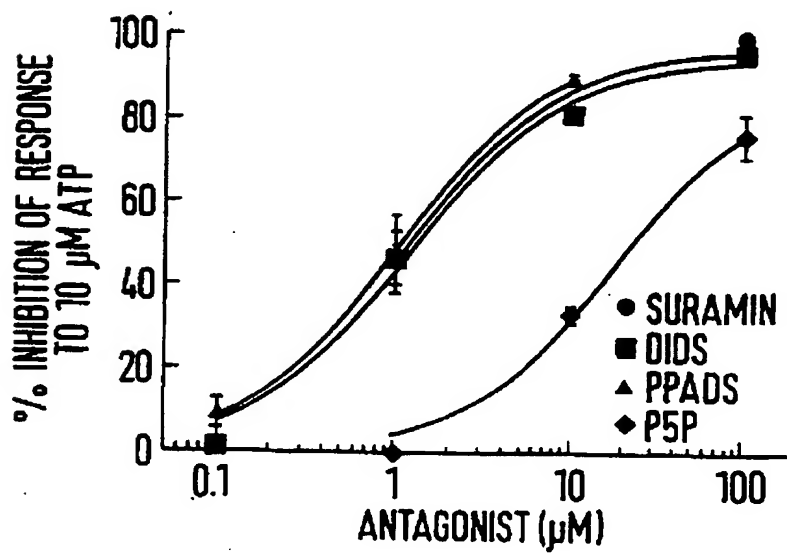
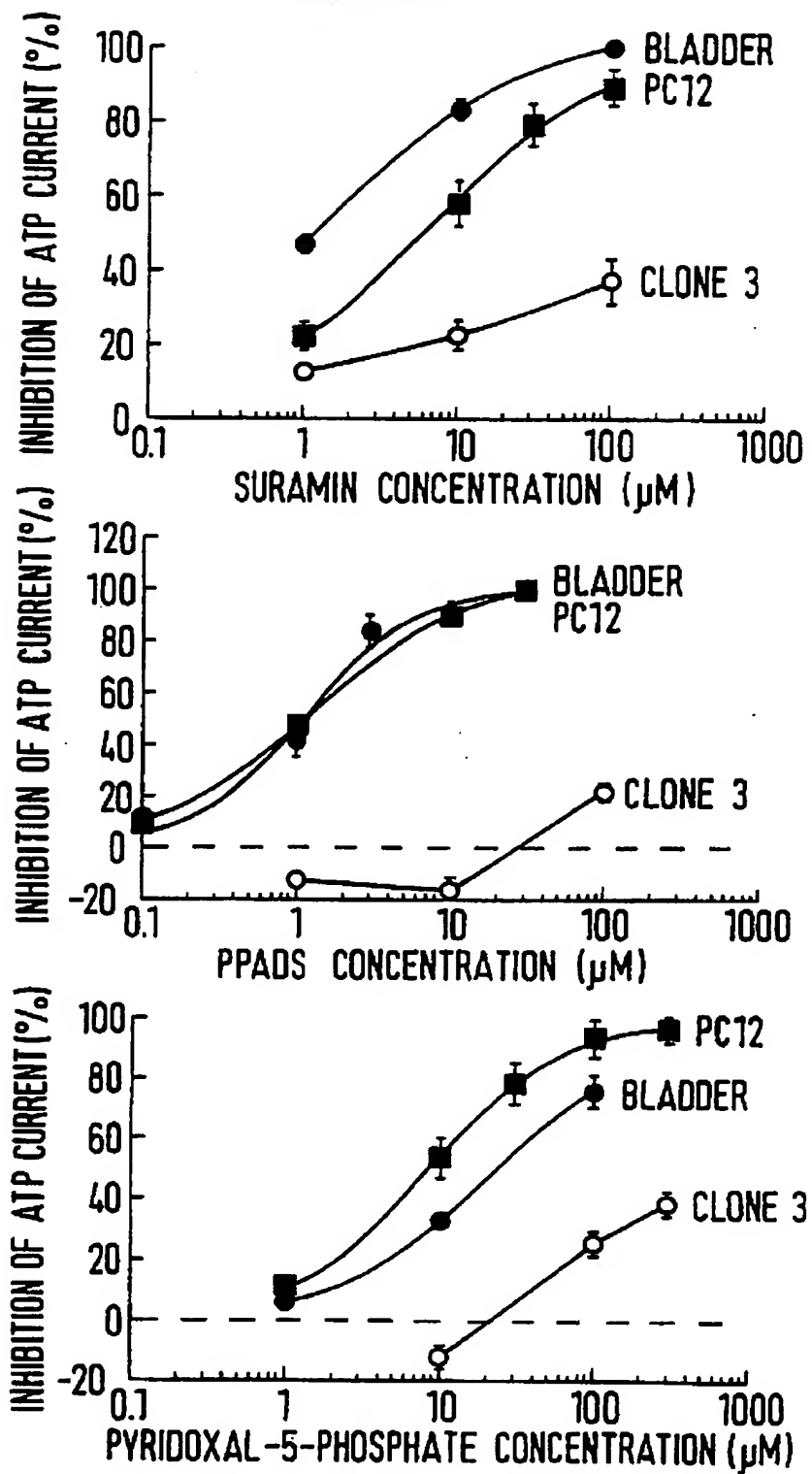


FIGURE 13



14 / 15

FIGURE 14



15 / 15

FIGURE 15

